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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 05:06:55 ; Search time 2053 Seconds
(without alignments)
822.840 Million cell updates/sec

Title: US-10-001-254-5
Perfect score: 294
Sequence: 1 acatattgctgcgcctcctca.....tgcctccagatgcgtccccc 294

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	294	100.0	294	14	US-10-001-254-5
2	294	100.0	1383	14	US-10-001-254-15
3	294	100.0	2817	10	US-09-966-451-3
4	294	100.0	2817	14	US-10-001-254-27
5	294	100.0	2817	16	US-10-630-399-3
6	294.4	99.5	1383	9	US-09-795-595-2
7	294.4	99.5	1383	10	US-09-759-595-2
8	241.6	82.2	501	9	US-09-833-790-149
9	204.4	69.5	1542	9	US-09-795-595-4
10	204.4	69.5	1542	10	US-09-759-595-4
11	151.8	51.6	31000	10	US-09-966-451-10
12	151.8	51.6	31000	16	US-10-630-399-10

13	137.6	46.8	211	14	US-10-001-254-25	Sequence 25, Appl
14	137.6	46.8	470	16	US-10-242-535A-26096	Sequence 26096, A
15	137.6	46.8	470	16	US-10-085-783A-26096	Sequence 26096, A
16	104.8	35.6	408	11	US-09-969-034-428	Sequence 428, App
17	43.2	14.7	256493	13	US-10-087-192-1000	Sequence 1000, Ap
18	42.6	14.5	1694	18	US-10-422-522-27	Sequence 27, Appl
19	42.6	14.5	2378	18	US-10-357-930-23166	Sequence 23166, A
20	42.6	14.5	2378	18	US-10-357-930-29035	Sequence 29035, A
21	40.4	13.7	2024	9	US-09-895-752-51	Sequence 51, Appl
22	40.4	13.7	2024	9	US-09-887-586A-51	Sequence 51, Appl
23	40.4	13.7	2024	9	US-09-903-012-51	Sequence 51, Appl
24	40.4	13.7	2024	10	US-09-900-797-51	Sequence 51, Appl
25	40.4	13.7	2024	11	US-09-893-820-51	Sequence 51, Appl
26	39.6	13.5	628	18	US-10-468-488-12	Sequence 12, Appl
27	37	12.6	399	18	US-10-674-124A-9403	Sequence 9403, Ap
28	37	12.6	126413	13	US-10-087-192-1831	Sequence 1831, Ap
29	36	12.2	2000	9	US-09-938-842A-4518	Sequence 4518, Ap
30	36	12.2	2000	11	US-09-938-842A-4518	Sequence 4518, Ap
31	35	11.9	2703	16	US-10-282-122A-40657	Sequence 40657, A
32	34.6	11.8	504	18	US-10-425-115-154005	Sequence 154005, A
33	34.4	11.7	131673	18	US-10-282-122A-27393	Sequence 27393, Ap
34	33.8	11.5	3879	16	US-09-960-870-2	Sequence 2, Appl1
35	33.8	11.5	22684	10	US-09-960-858-2	Sequence 2, Appl1
36	33.8	11.5	22684	10	US-10-251-668-2	Sequence 2, Appl1
37	33.8	11.5	22684	16	US-10-251-668-2	Sequence 1, Appl1
38	33.8	11.5	580073	15	US-10-205-220-1	Sequence 13505, A
39	33.6	11.4	1250	16	US-10-425-114-13505	Sequence 13505, A
40	33.6	11.4	1450	18	US-10-425-115-181981	Sequence 181981, Ap
41	33.6	11.4	2393	8	US-09-769-787-287	Sequence 287, App
42	33.6	11.4	2393	16	US-10-158-864-90	Sequence 90, Appl
43	33.6	11.4	2393	16	US-10-158-864-90	Sequence 5341, Ap
44	33.4	11.4	548	18	US-10-723-860-5341	Sequence 5341, Ap
45	33.2	11.3	899	14	US-10-198-846-7068	Sequence 7068, Ap

ALIGNMENTS

RESULT 1
US-10-001-254-5
; Sequence 5, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loreana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Steiner-Lieman, Frank
; TITLE OR INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCES: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(294)
US-10-001-254-5

Query Match 100.0%; Score 294; DB 14; Length 294;
Best Local Similarity 100.0%; Pred. No. 5; 4e-75;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 60
DB 1 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 60
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 120
DB 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 120
QY 121 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 180
DB 121 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 180
QY 181 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 240
DB 181 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 240
QY 241 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
DB 241 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294

RESULT 2

US-10-001-254-15
Sequence 15, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roch, Wilfred
APPLICANT: Stenmer-Liwen, Frank
TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1380)
US-10-001-254-15

Query Match 100.0%; Score 294; DB 14; Length 1383;
Best Local Similarity 100.0%; Pred. No. 1.1e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 60
DB 25 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 84
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 120
DB 85 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 144
QY 121 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 180
DB 145 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 204
QY 181 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 240
DB 205 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 264
QY 241 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294

DB 265 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 318

RESULT 3

US-09-966-451-3
Sequence 3, Application US/09966451
Publication No. US20030087856A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
FILE REFERENCE: R1S-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1432)
US-09-966-451-3

Query Match 100.0%; Score 294; DB 10; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 60
DB 74 ACATATGTCGCTGCTCAATGTTGACTAATAGGAAGCTGTCAGATTATTAATGATCCT 133
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 120
DB 134 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTATTAATAAACCATCTGGATGATAGATAC 193
QY 121 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 180
DB 194 AATCAGTTTCACATTAAGAGATTTTGAAGCACTTCAATCTGGAAGAAAAGTCCCACTTCT 253
QY 181 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 240
DB 254 GAATTAAGTTGACTGCGGACCAACAATTCACAGTTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
DB 314 ATCCAAATGAATTTTGTCTGCTGAGTCTTTTGTCTCCCGAGATGCTGTTCC 367

RESULT 4

US-10-001-254-27
Sequence 27, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roch, Wilfred
APPLICANT: Stenmer-Liwen, Frank
TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27

LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50) ... (1429)
US-10-001-254-27

Query Match 100.0%; Score 294; DB 14; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 60
DB ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 133
QY 61 CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 120
DB CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 193
QY 121 AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 180
DB AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 253
QY 194 AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 253
DB 181 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 240
DB 254 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 367

RESULT 5

US-10-630-399-3
Sequence 3, Application US/10630399
Publication No. US20040019009A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
FILE REFERENCE: RUS-0324
CURRENT APPLICATION NUMBER: US/10/630,399
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/966,451
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50) ... (1429)
US-10-630-399-3

Query Match 100.0%; Score 294; DB 16; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 60
DB ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 133
QY 61 CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 120
DB CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 193
QY 121 AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 180
DB AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 253
QY 181 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 240

DB 254 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 367

RESULT 6

US-09-795-595-2
Sequence 2, Application US/09795595
Publication No. US20020039423A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
OTHER INFORMATION: cDNA
NAME/KEY: CDS
LOCATION: (1) ... (1383)
OTHER INFORMATION: human IRAK-4
US-09-795-595-2

Query Match 99.5%; Score 292.4; DB 9; Length 1383;
Best Local Similarity 99.7%; Pred. No. 3.2e-74;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 60
DB ACATATGCGCGCTCCCTCAATGTTGAGTAACTAGGAGCTGTGAGATTTTATTGATCCT 84
QY 61 CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 120
DB CAAGAAGATGGAAGAGTTAGCTGTGACTTAAACCATCTGTGTGATGATGATAC 144
QY 121 AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 180
DB AATGAGTTTCATPAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 204
QY 181 GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 240
DB GAATTACTGTTGACTGGGACCAAAATTGACAGTTGTGATCTTGTGATCTTTTG 264
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 294
DB 265 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 318

RESULT 7

US-09-759-595-2
Sequence 2, Application US/09759595
Publication No. US20030059916A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
NAME/KEY: CDS
LOCATION: (1)..(1383)
OTHER INFORMATION: human IRAK-4
US-09-759-595-2

Query Match 99.5%; Score 292.4; DB 10; Length 1383;
Best Local Similarity 99.7%; Pred. No. 3.2e-74;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 60
DB 25 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 84
QY 61 CAAGAAGATGAGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 120
DB 85 CAAGAAGATGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 144
QY 121 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 180
DB 145 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 204
QY 181 GAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTTG 240
DB 205 GAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTTG 264
QY 241 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGAGTCTGTTCC 294
DB 265 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGAGTCTGTTCC 318

RESULT 8
US-09-833-790-149
Sequence 149, Application US/09833790
Patent No. US20020068288A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tonglong
APPLICANT: Secrist, Heather
APPLICANT: Mohamach, Radoch
APPLICANT: Indrias, Carol Y.
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 4.0.
SEQ ID NO 149
LENGTH: 501
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(501)
OTHER INFORMATION: n = A,T,C or G
US-09-833-790-149

Query Match 82.2%; Score 241.6; DB 9; Length 501;
Best Local Similarity 97.3%; Pred. No. 1.1e-59;
Matches 288; Conservative 0; Mismatches 4; Indels 4; Gaps 4;

QY 1 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 60
DB 45 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 104
QY 61 CAAGAAGATGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 120
DB 105 CAAGAAGATGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 164
QY 121 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 179
DB 165 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 223
QY 180 TGAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTT 238
DB 224 TGAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTT 283
QY 239 TGAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTT 294
DB 284 TGAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTT 338

RESULT 9
US-09-795-595-4
Sequence 4, Application US/09795595
Publication No. US20020039423A1
GENERAL INFORMATION:
APPLICANT: Mesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularix Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1542
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
NAME/KEY: CDS
LOCATION: (163)..(1542)
OTHER INFORMATION: murine IRAK-4
US-09-795-595-4

Query Match 69.5%; Score 204.4; DB 9; Length 1542;
Best Local Similarity 81.0%; Pred. No. 1.1e-48;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 60
DB 187 ACATATGCGCTGCTCAATGTTGACTAATAGAGAGCTGCAGATTTTATGATCCT 246
QY 61 CAAGAAGATGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 120
DB 247 CAAGAAGATGAGAGAGTGTAGCTGTAGCTATTAACCATCTGCTGATGATAGATAC 306
QY 121 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 180
DB 307 AATCAGTTTCACATTAAGAGATTTGAGAGCTTACTTCAACTGGAAGAGTCCACTTCT 366
QY 181 GAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTTG 240
DB 367 GAATTAAGTGTGAGCTGGGACCAACAATTGACAGTGGTATCTTGTGATCTTTG 426
QY 241 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGAGTCTGTTCC 294
DB 427 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGAGTCTGTTCC 480


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RESULT 10
US-09-759-595-4
; Sequence 4, Application US/09759595
; Publication No. US20030059916x1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
; US-09-759-595-4

Query Match          69.5%; Score 204.4; DB 10; Length 1542;
Best Local Similarity 81.0%; Pred. No. 1.1e-48;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGTGCGCTCCTCAATGTTGAGCTAATTAAGAAAGCTGTCAGATTTTATTGATCTT 60
DB 187 ACATACATAGCGCAACCTTAATGTGGGATCTCTAGGAAGCTGTGGATTTTATTGATCTT 246
QY 61 CAAGAAAGATGGAAGAGTTAGCTGTAGCTTTTAAAAAACCATCTGTGATGATGATAC 120
DB 247 CAAGAAAGGTTGAAGAAATTAGCAGTACTTCAAAAAAGCCGTCCGGGACAGACGATAC 306
QY 121 AATGATTTCACTAAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCT 180
DB 307 AATGATTTCACTAAGAGATTTGAAGCATTTACTTCAAGCCGGAGAGAGCCCACTTCT 366
QY 181 GAATTAAGTTGAGCTGGGACCAAAATTGACAGTTGATGATCTTTGATCTTTTG 240
DB 367 GAATGCTGTTGACCTGGGACCAAGCAAGTGGGACGACCTTTGATCTTACTG 426
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 294
DB 427 GTCCAGATGAGCTGTTTGTCCCGCCACTCTCTGCTGCGAGATGCGTTCCC 480

RESULT 11
US-09-966-451-10
; Sequence 10, Application US/09966451
; Publication No. US20030087856x1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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US-09-966-451-10
Query Match          51.6%; Score 151.8; DB 10; Length 31000;
Best Local Similarity 95.7%; Pred. No. 7.9e-33;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCAGTTTCAATAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGA 182
DB 12953 TTACTTACTTTTAAAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGA 13012
QY 183 ATTACTGTTGACCTGGGACCAAAATTGACAGTTGATCTTTGATCTTTGAT 242
DB 13013 ATTACTGTTGACCTGGGACCAAAATTGACAGTTGATCTTTGATCTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGAT 285
DB 13073 CCAAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGAT 13115

RESULT 12
US-10-630-399-10
; Sequence 10, Application US/10630399
; Publication No. US20040019009x1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/10/630,399
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/966,451
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Query Match          51.6%; Score 151.8; DB 16; Length 31000;
Best Local Similarity 95.7%; Pred. No. 7.9e-33;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCAGTTTCAATAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGA 182
DB 12953 TTACTTACTTTTAAAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGA 13012
QY 183 ATTACTGTTGACCTGGGACCAAAATTGACAGTTGATCTTTGATCTTTGAT 242
DB 13013 ATTACTGTTGACCTGGGACCAAAATTGACAGTTGATCTTTGATCTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGAT 285
DB 13073 CCAAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGAT 13115

RESULT 13
US-10-001-254-25
; Sequence 25, Application US/10001254
; Publication No. US20030049702x1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Steiner-Hilgen, Frank
; TITLE OF INVENTION: No. US20030049702x1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
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PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 211
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(177)
US-10-001-254-25

Query Match 46.8%; Score 137.6; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 1e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 60
DB 25 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 84
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 120
DB 85 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 144
QY 121 AATCAGTTTCACATTAAGAGATT 144
DB 145 AATCAGTTTCACATTAAGATGCTGT 168

RESULT 14

US-10-242-535A-26096
Sequence 26096, Application US/10242353A
Publication No. US2004001363A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26096
LENGTH: 470
TYPE: DNA
ORGANISM: Human
US-10-242-535A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;
Best Local Similarity 97.2%; Pred. No. 1.5e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 60
DB 139 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 198
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 120
DB 199 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 258
QY 121 AATCAGTTTCACATTAAGAGATT 144

DB 259 AATCAGTTTCACATTAAGATGCTGT 282

RESULT 15

US-10-085-783A-26096
Sequence 26096, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26096
LENGTH: 470
TYPE: DNA
ORGANISM: Human
US-10-085-783A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;
Best Local Similarity 97.2%; Pred. No. 1.5e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 60
DB 139 ACATATGTCGCTGCTCAATGTTGACTAATTAGAACTGTCAGATTTTATTGATCCT 198
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 120
DB 199 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATAGATAC 258
QY 121 AATCAGTTTCACATTAAGAGATT 144
DB 259 AATCAGTTTCACATTAAGATGCTGT 282

Search completed: January 12, 2005, 07:07:01
Job time : 2055 secs

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 04:23:14 ; Search time 75 Seconds
(without alignments)
2786.292 Million cell updates/sec

Title: US-10-001-254-5

Perfect score: 294
Sequence: 1 acatcgtgcgcgtcctca.....tgcctccagatcgtcc 294

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/Backfillseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294	100.0	833	US-09-166-350-10	Sequence 10, Appl
2	294	100.0	2817	US-09-966-451-3	Sequence 3, Appl
3	151.8	51.6	31000	US-09-966-451-10	Sequence 10, Appl
4	40.4	13.7	1879	US-09-601-091-1	Sequence 1, Appl
5	40.4	13.7	2024	US-09-601-091-3	Sequence 3, Appl
6	40.4	13.7	2024	US-09-398-395A-51	Sequence 51, Appl
7	40.4	13.7	2024	US-09-887-586A-51	Sequence 51, Appl
8	40.4	13.7	2024	US-09-895-752-51	Sequence 51, Appl
9	40.4	13.7	2024	US-09-903-012B-51	Sequence 51, Appl
10	40.4	13.7	2024	US-09-900-797-51	Sequence 51, Appl
11	38.2	13.0	267	US-09-543-681A-1549	Sequence 1549, Ap
12	33.8	11.5	580073	US-08-545-528D-1	Sequence 1, Appl
13	33.6	11.4	711	US-09-583-110-1653	Sequence 1653, Ap
14	33.6	11.4	2393	US-08-961-527-90	Sequence 90, Appl
15	33.2	11.3	654	US-09-248-796A-236	Sequence 236, App
16	33	11.2	640681	US-09-790-988-1	Sequence 1, Appl
17	32.8	11.2	477	US-09-513-999C-12039	Sequence 32039, A
18	32.8	11.2	202001	US-09-734-674-3	Sequence 3, Appl
19	32.6	11.1	1728	US-09-096-731A-1	Sequence 1, Appl
20	32.6	11.1	2971	US-09-710-279-3449	Sequence 3449, Ap
21	32.4	11.0	1737	US-09-248-796A-2516	Sequence 2516, Ap
22	32.4	11.0	98844	US-09-791-211-10	Sequence 10, Appl
23	32.2	11.0	4402	US-09-484-970B-135	Sequence 135, App
24	32	10.9	2274	US-09-107-532A-3535	Sequence 3535, Ap
25	32	10.9	3012	US-09-976-594-422	Sequence 422, App
26	32	10.9	3012	US-09-919-039-167	Sequence 167, App
27	32	10.9	9834	US-08-956-171E-37	Sequence 37, Appl

C	28	32	10.9	9834	4	US-08-781-986A-37	Sequence 37, Appl
	29	31.8	10.8	1545	4	US-09-710-279-2681	Sequence 2681, Ap
	30	31.8	10.8	1557	3	US-09-134-001C-1614	Sequence 1614, Ap
	31	31.8	10.8	2507	4	US-09-620-312D-120	Sequence 120, App
C	32	31.8	10.8	3247	4	US-09-710-279-3771	Sequence 3771, Ap
	33	31.8	10.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
	34	31.8	10.8	1664976	4	US-09-692-570-1	Sequence 1, Appl
	35	31.4	10.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
C	36	31.4	10.7	3320	4	US-09-710-279-3337	Sequence 3337, Ap
	37	31.4	10.7	3454	4	US-09-710-279-3998	Sequence 3998, Ap
C	38	31.4	10.7	4045	4	US-09-710-279-3929	Sequence 3929, Ap
	39	31.4	10.7	12720	2	US-08-403-866-11	Sequence 11, Appl
	40	31	10.5	2126	2	US-08-545-745-1	Sequence 1, Appl
C	41	30.8	10.5	224	4	US-09-513-999C-11151	Sequence 11151, A
	42	30.8	10.5	708	4	US-09-248-796A-6765	Sequence 6765, Ap
	43	30.8	10.5	1056	4	US-09-134-000C-1031	Sequence 1031, Ap
	44	30.8	10.5	1161	4	US-09-976-594-423	Sequence 423, App
	45	30.8	10.5	1550	4	US-09-427-501-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-166-350-10
; Sequence 10, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: 10461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-10

Query Match      100.0%; Score 294; DB 4; Length 833;
Best Local Similarity 100.0%; Pred. No. 1,1e-82;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAAGAGCTGTCAGATTATGATCCT 60
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DB 74 ACATATGTCGCTGCTCAATGTTGACTAATTAAGAGCTGTCAGATTATGATCCT 133
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QY 61 CAAGAGATGGAAGAGATTGCTGTACTTTTAAAAACATCTGGTGAATGATAC 120
    |||||
DB 134 CAAGAGATGGAAGAGATTGCTGTACTTTTAAAAACATCTGGTGAATGATAC 193
    |||||

QY 121 AATCAGTTTCATTAAGAGATTGAGCATTTACTTCAACTGGAAGAGTCCACTCT 180
    |||||
DB 194 AATCAGTTTCATTAAGAGATTGAGCATTTACTTCAACTGGAAGAGTCCACTCT 253
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QY 181 GAATTAATGTTGACTGCGGACCAAAATTCACAGTTGTGATCTTGTGATCTTTTG 240
    |||||
DB 254 GAATTAATGTTGACTGCGGACCAAAATTCACAGTTGTGATCTTGTGATCTTTTG 313
    |||||

QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
    |||||
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367
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RESULT 2
US-09-966-451-3
; Sequence 3, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1432)
US-09-966-451-3

Query Match
Best Local Similarity 100.0%; Score 294; DB 4; Length 2817;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCATATGTTGAGTAAATGAAAGCTGTGAGATTTTATGATCCT 60
DB 74 ACATATGTCGCTGCTCATATGTTGAGTAAATGAAAGCTGTGAGATTTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAGTTAGTGTGCTATTTAAATCAATCTGTTGATGATGATAC 120
DB 134 CAAGAAGATGGAAGAGTTAGTGTGCTATTTAAATCAATCTGTTGATGATGATAC 193
QY 121 AATCAGTTTCATATGAGAGATTTGAAGCATTTACTTAACTGGAATAAGTCCACTCT 180
DB 194 AATCAGTTTCATATGAGAGATTTGAAGCATTTACTTAACTGGAATAAGTCCACTCT 253
QY 181 GAATTTACTGTTTGAAGTGGGACACCAATTTGCAAGTTGATCTTTGATCTTTTG 240
DB 254 GAATTTACTGTTTGAAGTGGGACACCAATTTGCAAGTTGATCTTTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCGAGTCTTTTGTCCCAAGTGTGTTCC 294
DB 314 ATCCAAATGAATTTTGTCTCGAGTCTTTTGTCCCAAGTGTGTTCC 367

RESULT 3
US-09-966-451-10
; Sequence 10, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-966-451-10

Query Match
Best Local Similarity 51.6%; Score 151.8; DB 4; Length 31000;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCAGTTTCATATGAGAGATTTGAAGCATTTCTTAAATGGAATAAGTCCACTTTCGA 182
DB 12953 TTACTTACTTTTAAGAGATTTGAAGCATTTCTTAAATGGAATAAGTCCACTTTCGA 13012

QY 183 ATTACTGTTTACTGAGGACCAACAAATTCACAGTTGTGATCTTGATCTTTGAT 242
DB 13013 ATTACTGTTTACTGAGGACCAACAAATTCACAGTTGTGATCTTGATCTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTTCCGAGTCTTTTGTCTCCCAAT 285
DB 13073 CCAAAATGAATTTTGTCTTCCGAGTCTTTTGTCTCCCAAGT 13115

RESULT 4
US-09-601-091-1
; Sequence 1, Application US/09601091
; Patent No. 6342380
; GENERAL INFORMATION:
; APPLICANT: Colby, S. M. et al.
; TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon Esculentum
; FILE REFERENCE: 4630-55758
; CURRENT APPLICATION NUMBER: US/09/601,091
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/US99/02133
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: US 60/073,579
; PRIOR FILING DATE: 1998-02-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)...(1685)
US-09-601-091-1

Query Match
Best Local Similarity 13.7%; Score 40.4; DB 3; Length 1879;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 45 AAGATTATATGATCTCTCAAGAGATGGAAGAACTGCTGTGCTATTTAAATCAATC 104
DB 761 AAGCTTGTGATCTCTCAAGAGATGGAAGAACTGCTGTGCTATTTAAATCAATC 820
QY 105 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
DB 821 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 880
QY 165 AAAAGTCCACTTCTGATTTACTGTTTGAAGTGGGACCAACAAATTCACAGTTGTG 224
DB 881 AATAGTGTGCGGAGAAATGATGACAAAGTACTAACCTGACTCATTTATGACGA 940
QY 225 TCTTGTGATCTTT 238
DB 941 CACTTTGATGCTT 954

RESULT 5
US-09-601-091-3
; Sequence 3, Application US/09601091
; Patent No. 6342380
; GENERAL INFORMATION:
; APPLICANT: Colby, S. M. et al.
; TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon Esculentum
; FILE REFERENCE: 4630-55758
; CURRENT APPLICATION NUMBER: US/09/601,091
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/US99/02133
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: US 60/073,579
; PRIOR FILING DATE: 1998-02-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1678)
US-09-601-091-3

Query Match 13.7% Score 40.4; DB 3; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 45 AGATTATTTAGTCTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGGATTTCGAATTAATATCCATA 813
QY 105 TGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 164
DB 814 TGCAAGACAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
QY 165 AAAAGTCCCACTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 224
DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCAACTGACCTCAATTAATTAAT 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 6
US-09-398-395A-51
Sequence 51, Application US/09398395A
Patent No. 6468772
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64687721, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 51
LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1675)
OTHER INFORMATION: VENT germacrene C synthase
US-09-398-395A-51

Query Match 13.7% Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTATTTAGTCTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGGATTTCGAATTAATATCCATA 813
QY 105 TGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 164
DB 814 TGCAAGACAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
QY 165 AAAAGTCCCACTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 224

DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCAACTGACCTCAATTAATTAAT 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 7
US-09-887-586A-51
Sequence 51, Application US/09887586A
Patent No. 6495354
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 51
LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1675)
OTHER INFORMATION: VENT germacrene C synthase
US-09-887-586A-51

Query Match 13.7% Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTATTTAGTCTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGGATTTCGAATTAATATCCATA 813
QY 105 TGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 164
DB 814 TGCAAGACAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
QY 165 AAAAGTCCCACTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 224
DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCAACTGACCTCAATTAATTAAT 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 8
US-09-895-752-51
Sequence 51, Application US/09895752
Patent No. 6559297
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 65592971, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 2001-06-29

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;; PRIOR APPLICATION NUMBER: 09/398,395
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 51
;; LENGTH: 2024
;; TYPE: DNA
;; ORGANISM: Lycopersicon esculentum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (32)...(1675)
;; OTHER INFORMATION: VFNT germacrene C synthase
US-09-895-752-51
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```
Query Match      13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
```

```
Oy 45 AGATTTTATGATCTCCAGAGAGATGAGAGATTAGCTGATTTAAACATC 104
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Db 754 AGAGCTTAGTGAATCTTACAGAGTGGTGGAGAAAGATTGGCAATTAATTCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGATTCTCAACTGG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGCAAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCGAGAAAATGATGACAAAAGTACTGACCTGCTCATTTATGAGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 9
US-09-903-012B-51
;; Sequence 51, Application US/09903012B
;; Patent No. 6569656
;; GENERAL INFORMATION:
;; APPLICANT: Chappell, Joseph
;; APPLICANT: No. 6569656, Joseph P.
;; APPLICANT: Starks, Courtney M.
;; APPLICANT: Manna, Kathleen R.
;; TITLE OF INVENTION: SYNTHASES
;; FILE REFERENCE: 07678-025001
;; CURRENT APPLICATION NUMBER: US/09/903,012B
;; CURRENT FILING DATE: 2001-07-11
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 51
;; LENGTH: 2024
;; TYPE: DNA
;; ORGANISM: Lycopersicon esculentum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (32)...(1675)
;; OTHER INFORMATION: VFNT germacrene C synthase
US-09-903-012B-51
```

```
Query Match      13.7%; Score 40.4; DB 4; Length 2024;
```

```
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Oy 45 AGATTTTATGATCTCCAGAGAGATGAGAGATTAGCTGATTTAAACATC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 AGAGCTTAGTGAATCTTACAGAGTGGTGGAGAAAGATTGGCAATTAATTCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGATTCTCAACTGG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGCAAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCGAGAAAATGATGACAAAAGTACTGACCTGCTCATTTATGAGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
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```

```
RESULT 10
US-09-900-797-51
;; Sequence 51, Application US/0990797
;; Patent No. 6645762
;; GENERAL INFORMATION:
;; APPLICANT: Chappell, Joseph
;; APPLICANT: No. 6645762, Joseph P.
;; APPLICANT: Starks, Courtney M.
;; APPLICANT: Manna, Kathleen R.
;; TITLE OF INVENTION: SYNTHASES
;; FILE REFERENCE: 07678-025001
;; CURRENT APPLICATION NUMBER: US/09/900,797
;; CURRENT FILING DATE: 2001-07-06
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 51
;; LENGTH: 2024
;; TYPE: DNA
;; ORGANISM: Lycopersicon esculentum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (32)...(1675)
;; OTHER INFORMATION: VFNT germacrene C synthase
US-09-900-797-51
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```
Query Match      13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
```

```
Oy 45 AGATTTTATGATCTCCAGAGAGATGAGAGATTAGCTGATTTAAACATC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 AGAGCTTAGTGAATCTTACAGAGTGGTGGAGAAAGATTGGCAATTAATTCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGATTCTCAACTGG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGCAAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCGAGAAAATGATGACAAAAGTACTGACCTGCTCATTTATGAGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 11
```

	Query Match	Similarity	11.5%	Score 33.8	DB 4	Length 580073
	Best Local	Similarity	53.4%	Pred. No. 9		
	Matches	71	Conservative	0	Mismatches 62	Indels 0
					Gaps	0
Qy	143	TTGAAGCATTTACTTCAACCTGGAAGAAAGTCCCACTCTGAATTAATCTGTTGACTGGGGCA	202			
Db	431703	TTGAAGCATTTGTTGAAACCAAAACCAAACTCTGATGATGATCATTAATTGACAGATTG	431644			
Qy	203	CCACAAATTGCACAGTGTGTAATCTTTGGATCTTTTGATCCAAATGAATTTTTTGCTC	262			
Db	431643	TTAATCGCTACCAATTACTCTATAGTTGATCTGAACACAAAAAATATTGTAGAG	431584			
Qy	263	CTGGAGTCTTTT	275			
Db	431583	CTAAGTCTTAAT	431571			

1 GENERAL INFORMATION:
2 APPLICANT: Charles Kunsch
3 TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
4 NUMBER OF SEQUENCES: 391
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Human Genome Sciences, Inc.
7 STREET: 9410 Key West Avenue
8 CITY: Rockville
9 STATE: Maryland
0 COUNTRY: USA
1 ZIP: 20850
2
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
5 COMPUTER: HP Vectra 486/33
6 OPERATING SYSTEM: MSDOS version 6.2
7 SOFTWARE: ASCII Text
8
9 CURRENT APPLICATION DATA:
0 APPLICATION NUMBER: US/08/961,527
1
2 FILING DATE:
3 CLASSIFICATION: 424
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER:
6
7 FILING DATE:
8
9 ATTORNEY/AGENT INFORMATION:
0

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 2393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-90

Search completed: January 12, 2005, 05:40:47
Job time : 90 secs

Query Match

Best Local Similarity 11.4%; Score 33.6; DB 4; Length 2393;
Matches 90; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 37 AAGCTGTCAGATTTTATTTGATCCTCAGAGAAGATGAGAAGTTAGCTGATTTAA 96
DB 1113 AACCTTTAGTACCAAGCACTAAAGAGCTGCACAAAGAGATATTCCTATTAG 1054
QY 97 AAACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 156
DB 1053 ATAGGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 994
QY 157 CAACTGGAAGAAAGTCCCACTTCTGATTAAGTTGATGATGATGATGATGAT 216
DB 993 GTTACTCTAAGAAATATCTGCTAATTTGCAATATATGAGAGACTAACAATTGACA 934
QY 217 GTTG 220
DB 933 AATG 930

RESULT 15

US-09-248-796A-236
; Sequence 236, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 236
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-236

Query Match 11.3%; Score 33.2; DB 4; Length 654;
Best Local Similarity 51.3%; Pred. No. 0.74; 73; Indels 0; Gaps 0;

Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 85 GTAGCTATTAAAAAACCATCTGATGATGATGATGATGATGATGATGATGAT 144
DB 226 GTAGCATCAAGACACGACGACGCCGTTAAGTTGATGATGATGATGATGAT 285
QY 145 GAAGCATTTACTCAAACTGAGAAAAGTCCCACTTCTGAATTAAGTTGATGAT 204
DB 286 GCAAAATTATGAGAGTTTGAAGAACCACTTGAATTAAGTTAACAAGCAGCT 345
QY 205 ACAATTGACAGTTGATGATGATGATGATGATGATGATGATGATGATGAT 234
DB 346 AAGTATGATCTCAATGTTGTTACCAAGAT 375

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:33:48 ; Search time 1934 Seconds

(without alignments)
5539,442 Million cell updates/sec

Title: US-10-001-254-5

Perfect score: 294

Sequence: 1 acatcatgtgcgtcgtcctcaaa.....tgcctccagatcgtctccc 294

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	100.0	859	4	BG164491 602342026
2	292.4	99.5	811	4	BG164438 602642772
3	273.2	92.9	821	7	CK459029 923479 WA
4	267.2	90.9	719	2	BF696981 602130160
5	262.2	89.1	402	2	BE482619 168463 BA
6	262	89.1	666	7	CN788062 4122347 B
7	261	88.8	1383	9	AY418791 Homo sapi
8	258.4	87.9	1383	9	AY418792 Pan trogl
9	220	74.8	341	4	BG691069 340084 BA
10	205.4	69.9	313	4	BM151935 TCBAPE11
11	204.4	69.5	503	6	CA538859 C0272801
12	204.4	69.5	598	5	BO552228 HA014C09
13	204.4	69.5	637	2	BB660378 BB660378
14	204.4	69.5	637	2	BB613447 BB613447
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16	204.4	69.5	663	6	BY726858 BY726858
17	204.4	69.5	676	2	BB613167 BB613167
18	204.4	69.5	1161	3	AK020397 Mus muscu
19	204.4	69.5	2481	3	AK020397 Mus muscu
20	204.4	69.5	2810	3	AK020397 Mus muscu
21	202.8	69.0	575	5	BK522921 BK522921
22	198.8	67.6	265	2	AM436511 76774 MAR
23	182.4	62.0	507	2	BB866698 BB866698
24	182.2	62.0	1286	9	AY418793 Mus muscu

25	181.4	61.7	524	2	AM106160	AM106160 um23h11.Y
26	163.2	55.5	453	2	BB860349	BB860349 BB860349
27	154.2	52.4	686	7	CN066297	CN066297 F20_Ag2_P
28	154.2	52.4	711	7	CN067840	CN067840 K20_Ag2_P
29	154.2	52.4	775	7	CN061000	CN061000 A22_Ag2_P
30	154.2	52.4	782	7	CN064552	CN064552 Ag2_P_L2
31	147.6	50.2	852	5	BU209111	BU209111 603950834
32	144.4	49.1	600	1	AJ453616	AJ453616 AJ453616
33	144.4	49.1	670	1	AT447581	AT447581 AT447581
34	141.8	48.2	417	7	CO780006	CO780006 BL0088_H0
35	139.8	47.6	540	1	AL699213	AL699213 DKF2P86K
36	139.6	47.5	505	2	BE482323	BE482323 168064 BA
37	139.4	47.4	606	1	AL647125	AL647125 AL647125
38	139.2	47.3	625	9	CE224557	CE224557 t19r-g88-
39	137.6	46.8	284	1	AA114228	AA114228 znt5c05.r
40	137.6	46.8	753	6	CD654941	CD654941 AGENCOURT
41	137.6	46.8	783	7	CF596589	CF596589 AGENCOURT
42	134	45.6	576	2	BF238344	BF238344 601904613
43	125.8	42.0	270	2	BE845841	BE845841 234716 BA
44	123.4	42.0	664	4	BJ035962	BJ035962 BJ035962
45	114.4	38.9	599	4	BT691338	BT691338 BT691338

ALIGNMENTS

RESULT 1
LOCUS BG164491
DEFINITION 602342026F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4452055 5', mRNA sequence.
ACCESSION BG164491
VERSION BG164491.1 GI:12671194
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNAH10240 row: d column: 08
High quality sequence stop: 634.
Location/Qualifiers
1..859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4452055"
/issue_type="hypermethylation, cell line"
/lab host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_89"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

FEATURES

source

ORIGIN

Query Match 100.0%; Score 294; DB 4; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-70;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 60
 Db 59 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 118
 Qy 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAATAAACATCTGTGATGATGATAC 120
 Db 119 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAATAAACATCTGTGATGATGATAC 178
 Qy 121 AATCAGTTTCACATTAAGAGATTTGAAGCATTAATCTGCAAAAAGTCCACTTCT 180
 Db 179 AATCAGTTTCACATTAAGAGATTTGAAGCATTAATCTGCAAAAAGTCCACTTCT 238
 Qy 181 GAATTAAGTTGATCTGGGACCAACAATTTGACAGTTGGTATCTTGTGATCTTTTG 240
 Db 239 GAATTAAGTTGATCTGGGACCAACAATTTGACAGTTGGTATCTTGTGATCTTTTG 298
 Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 294
 Db 299 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 352

RESULT 2
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 LOCUS 602642772F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773760 5',
 DEFINITION mRNA sequence.

ACCESSION BG616438
 VERSION BG616438.1 GI:13667809
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.jnl.gov
 Plate: ILNL1645 row: P column: 17
 High quality sequence start: 3
 High quality sequence stop: 613.
 Location/Qualifiers

FEATURES

source

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4773760"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_1ib="NIH MGC 61"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccctggc); Site_2: SfiI (ggcgccatggc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGCGCGCGCGCGCATG-dt(30)BN-3',
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match

99.5%; Score 292.4; DB 4; Length 811;

Best Local Similarity 99.7%; Pred. No. 2.8e-70;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 60
 Db 77 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 136
 Qy 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAATAAACATCTGTGATGATGATAC 120
 Db 137 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAATAAACATCTGTGATGATGATAC 196
 Qy 121 AATCAGTTTCACATTAAGAGATTTGAAGCATTAATCTGCAAAAAGTCCACTTCT 180
 Db 197 AATCAGTTTCACATTAAGAGATTTGAAGCATTAATCTGCAAAAAGTCCACTTCT 256
 Qy 181 GAATTAAGTTGATCTGGGACCAACAATTTGACAGTTGGTATCTTGTGATCTTTTG 240
 Db 257 GAATTAAGTTGATCTGGGACCAACAATTTGACAGTTGGTATCTTGTGATCTTTTG 316
 Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 294
 Db 317 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 370

RESULT 3
 LOCUS CK459029 821 bp mRNA linear EST 14-JAN-2004
 DEFINITION 923479 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION CK459029
 VERSION CK459029.1 GI:40830310
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE
 AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 TITLE 1 (bases 1 to 821)
 JOURNAL Smith, T.P.L., Preking, B.A., Ford, J.J., Vallee, J.L., Wise, T.A.,
 Noneman, D.J., Wray, J.E. and Keeler, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TMM8032 row: K column: 23
 Seq primer: GTAATACAGCTCACTATAGG.
 Location/Qualifiers

FEATURES

source

1..821
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_1ib="MARC 4P1G"
 /note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match 92.9%; Score 273.2; DB 7; Length 821;
 Best Local Similarity 95.6%; Pred. No. 5.9e-65;
 Matches 281; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 60
 Db 233 ACATATGTCGCTGCTCAATGTTGAATTAATAGGAAGCTGCAATTTATATCTT 292

QY 61 CAAGAGAGTGAAGAGTAGTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 120
 DB 293 CAAGAGAGTGAAGAGTAGTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 352
 QY 121 AATCAGTTTCATATAGAGAGATTGAGCACTTACTTCAACTGAAAAAGTCCACTTCT 180
 DB 353 AACAGTTTCATATAGAGAGATTGAGCACTTACTTCAACTGAAAAAGTCCACTTCT 412
 QY 181 GAATTAAGTGTGATGAGGAGGACCAACAAATGACAGTTGATCTTGTGATCTTTT 240
 DB 413 GAATTAAGTGTGATGAGGAGGACCAACAAATGACAGTTGATCTTGTGATCTTTT 472
 QY 241 ATCCAAATGAATTTTGTCTCTGAGAGCTTTTGTCTCCAGAGTGTCTTCCC 294
 DB 473 GTCCAAAATGAATTTTGTCTCTGAGAGCTTTTGTCTCCAGAGTGTCTTCCC 526

RESULT 4
 BF696981 719 bp mRNA linear EST 22-DEC-2000
 LOCUS 602130160P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5',
 DEFINITION mRNA sequence.
 ACCESSION BF696981
 VERSION BF696981.1 GI:11982389
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 719)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LNCMI124 row: 9 column: 15
 High quality sequence stop: 632.
 Location/Qualifiers
 1. 719
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4287014"
 /tissue_type="Primitive neuroectoderm"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1lb="NIH_MGC_56"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccgccc); Site_2: SfiI (ggcgccgccc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGAGGCGGCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.9%; Score 267.2; DB 2; Length 719;
 Best Local Similarity 98.3%; Pred. No. 2.7e-63;
 Matches 291; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 1 ACATATGTGCGCTGCTCAATGTGAGTAAATTAAGAGCTGTGAGATTATTGATCT 60
 DB 92 ACATATGTGCGCTGCTCAATGTGAGTAAATTAAGAGCTGTGAGATTATTGATCT 151

QY 61 CAAGAGAGTGAAGAGTAGTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 120
 DB 152 CAAGAGAGTGAAGAGTAGTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 211
 QY 121 AATCAGTTTCATATAGAGAGATTGAGCACTTACTTCAACTGAAAAAGTCCACTTCT 180
 DB 212 AATCAGTTTCATATAGAGAGATTGAGCACTTACTTCAACTGAAAAAGTCCACTTCT 271
 QY 181 GAATTAAGTGTGATGAGGAGGACCAACAAATGACAGTTGATCTTGTGATCTTTT 239
 DB 272 GAATTAAGTGTGATGAGGAGGACCAACAAATGACAGTTGATCTTGTGATCTTTT 331
 QY 240 GATCCAAATGAATTTTGTCTCTGAGAGCTTTTGTCTCCAGAGTGTCTTCCC 294
 DB 332 GATCCAAATGAATTTTGTCTCTGAGAGCTTTTGTCTCCAGAGTGTCTTCCC 387

RESULT 5
 BE482619 402 bp mRNA linear EST 27-MAR-2003
 LOCUS 168463 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE482619
 ACCESSION BE482619
 VERSION BE482619.1 GI:9602152
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 402)
 Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
 Connor,E.B., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
 and Quackenbush,J.
 Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index
 Mamm. Genome 13 (7), 373-379 (2002)
 22135956
 12140684
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@ipst.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.
 PCR primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 11 row: F column: 7
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1. 402
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_1lb="BARC 5BOV"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

FEATURES
 source

ORIGIN

Query Match 89.1%; Score 262; DB 2; Length 402;
 Best Local Similarity 93.2%; Pred. No. 6.7e-62;
 Matches 274; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ACATATGTGCGCTGCTCAATGTGAGTAAATTAAGAGCTGTGAGATTATTGATCT 60
 DB 1 ACATATGTGCGCTGCTCAATGTGAGTAAATTAAGAGCTGTGAGATTATTGATCT 60

Db 88 ACATACGTCGCTGCTCCTGACATTAATTAGAAAGCTGCCGATTTTATGATCCT 147
 Qy 61 CAAGAAGATGAGAGATGAGTCTGCTAGCTTTTAAACCATCTGGATGATGATAC 120
 Db 148 CAAAGAGATGAGAGATGAGTCTGCTAGCTTTTAAACCATCTGGATGATGATAC 207
 Qy 121 AATCAGTTTCACATTAAGAGATTTGAGACATTAATCTCAACTGAAAAAGCCCACTCT 180
 Db 208 AATCAGTTTCACATTAAGAGATTTGAGACATTAATCTCAACTGAAAAAGCCCACTCT 267
 Qy 181 GAATTAAGTCTTTGACTGGGGGACCAACAATTCACAGTTGGTATCTTGGATCTTTTG 240
 Db 268 GAGTTACTGTTTGACTGGGGGACCAACAATTCACAGTTGGTATCTTGGATCTTTTG 327
 Qy 241 ATCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCC 294
 Db 328 GTCCAAATGAGTTTGTGCTGCGAGCTTTTGTCTCCAGATGCTGTACC 381

RESULT 6
 LOCUS CN788062 666 bp mRNA linear EST 26-MAY-2004
 DEFINITION 4122347 BARC 8BOV Bos taurus cDNA clone 8BOV_26007 5', mRNA
 sequence.
 ACCESSION CN788062
 VERSION CN788062.1 GI:47684042
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 666)
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and Matukumalli,L.K.
 Construction and Analysis of a cDNA Library Generated From Unpublished Muscle and Epithelial Tissues of Holstein Cattle
 JOURNAL Contract: Richard G. Baumann
 COMMENT Bovine Functional Genomics Lab
 ANRI BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744
 Email: rbaumann@nri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '-trim_faata. Vector identified by cross_match using options -mismatch 12 -mismatch 18
 Plate: 26 row: 0 column: 07
 Seg primer: CCTATTAGGTGACACTATAGAAC
 High quality sequence stop: 666.
 Location/Qualifiers

FEATURES
 source 1..666

/organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_26007"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B Tona"
 /clone_1ib="BARC 8BOV"
 /note="Organ: Intestine; Vector: pcwvSport6.1; Site: 1: NotI, Site 2: EcoRI; Normalized cow cDNA intestinal library in pcwvSport6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 89.1%; Score 262; DB 7; Length 666;

Best Local Similarity 93.2%; Pred. No. 7.3e-62;
 Matches 274; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 ACATATGTCGCTGCTCCTGACATTAATTAGAAAGCTGCCGATTTTATGATCCT 60
 Db 69 ACATATGTCGCTGCTCCTGACATTAATTAGAAAGCTGCCGATTTTATGATCCT 128
 Qy 61 CAAAGAGATGAGAGATGAGTCTGCTAGCTTTTAAACCATCTGGATGATGATAC 120
 Db 129 CAAAGAGATGAGAGATGAGTCTGCTAGCTTTTAAACCATCTGGATGATGATAC 188
 Qy 121 AATCAGTTTCACATTAAGAGATTTGAGACATTAATCTCAACTGAAAAAGCCCACTCT 180
 Db 189 AATCAGTTTCACATTAAGAGATTTGAGACATTAATCTCAACTGAAAAAGCCCACTCT 248
 Qy 181 GAATTAAGTCTTTGACTGGGGGACCAACAATTCACAGTTGGTATCTTGGATCTTTTG 240
 Db 249 GAGTTACTGTTTGACTGGGGGACCAACAATTCACAGTTGGTATCTTGGATCTTTTG 308
 Qy 241 ATCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCC 294
 Db 309 GTCCAAATGAGTTTGTGCTGCGAGCTTTTGTCTCCAGATGCTGTACC 362

RESULT 7
 LOCUS AY418791 1383 bp DNA linear GSS 17-DEC-2003
 DEFINITION Homo sapiens IRAK4 gene, VIRUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY418791
 VERSION AY418791.1 GI:3974751
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1383)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
 Interfering nonneutral evolution from human-chimp-mouse orthologous gene trilos

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1383)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
 Location/Qualifiers

FEATURES
 source 1..1383

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..51383
 /gene="IRAK4"
 /locus_tag="HOM6675"

ORIGIN

Query Match 88.8%; Score 261; DB 9; Length 1383;
 Best Local Similarity 88.8%; Pred. No. 1.6e-61;
 Matches 261; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 Qy 1 ACATATGTCGCTGCTCCTGACATTAATTAGAAAGCTGCCGATTTTATGATCCT 60
 Db 25 ACATATGTCGCTGCTCCTGACATTAATTAGAAAGCTGCCGATTTTATGATCCT 84

```

Qy 61 CAAGAAGATGGAAGATTAGCTGTGCTATTAAACCATCTGGNGATGATGATAC 120
Db 85 CAGAGAGATGGAAGATTAGCTGTGCTATTAAACCATCTGGNGATGATGATAC 144
Qy 121 AATCAGTTTCACATGAGAGATTGGAAGCATTACTTCAAACTGAAAAAGTCCACTTCT 180
Db 145 AATCAGTTTCACATGAGAGATTGGAAGCATTACTTCAAACTGAAAAAGTCCACTTCT 204
Qy 181 GAATTACTGTTTGACTGGGGACCACAAAATGCACTGTGTATCTTTGGATCTTTTG 240
Db 205 GAATTACTGTTTGACTGGGGACCACAAAATGCACTGTGTATCTTTGGATCTTTTG 264
Qy 241 ATCCAAATGAATTTTGTGCTCTGCGAGCTTTTGTCTCCAGATGCTTCCC 294
Db 265 ATCCAAATGAATTTTGTGCTCTGCGAGCTTTTGTCTCCAGATGCTTCCC 318

RESULT 8
AY418792 1383 bp DNA linear GSS 17-DEC-2003
LOCUS Pan troglodytes IRAK4 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY418792
VERSION AY418792.1 GI:39774752
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 1383)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14673302
2 (bases 1 to 1383)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..1383
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1383
/gene="IRAK4"
/locus_tag="HCM6675"

ORIGIN
Query Match 87.9%; Score 258.4; DB 9; Length 1383;
Best Local Similarity 88.1%; Pred. No. 8.3e-61;
Matches 259; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```

```

Qy 181 GAATTACTGTTTGACTGGGGACCACAAAATGCACTGTGTATCTTTGGATCTTTTG 240
Db 205 GAATTACTGTTTGACTGGGGACCACAAAATGCACTGTGTATCTTTGGATCTTTTG 264
Qy 241 ATCCAAATGAATTTTGTGCTCTGCGAGCTTTTGTCTCCAGATGCTTCCC 294
Db 265 ATCCAAATGAATTTTGTGCTCTGCGAGCTTTTGTCTCCAGATGCTTCCC 318

RESULT 9
BG691069 541 bp mRNA linear EST 27-MAR-2003
LOCUS BG691069
DEFINITION 340084 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG691069
VERSION BG691069.1 GI:13932889
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 541)
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,B.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Belg. 200 Km 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tad@lps1.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCAGTCACGACG
Plate: 100 row, B column: 15
Seq primer: ATTTAGCTGACACTATG.
Location/Qualifiers
1..541
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/contig="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/notes="Vector: pCMV SPORTE; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN
Query Match 74.8%; Score 220; DB 4; Length 541;
Best Local Similarity 93.9%; Pred. No. 3.2e-50;
Matches 229; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db	Accession	Version	Source	Organism	Reference Authors	Title	Journal	Comment
Db	ACATATGAGCGCCGCTCAATGTTGACATAATTAGGAAGCTGTCAAGATTATTATGATCCT	136						
Qy	61	CAAGAAGATGGAAGAAAGTTAGCTGTAGCTATTAAAAACCACTGGTGATGATAGATAC	120					
Db	137	CAAGAAAGATGGAAGAAAGTTAGCTGTAGCTATTAAAAACCATCTGGTGATGATAGATAC	196					
Qy	121	AATCAGTTTCACATTAAGAGATTGAGCATTTCAACTGAACTGGAAGAAAGCTCCACTTCT	180					
Db	197	AATCAGTTTCACATTAAGAGATTGAGCATTTCAACTGGAAGAAAGCTCCACTTCT	256					
Qy	181	GAATTACTGTGTTGACATGCGGGCAACCAATTGACACAGTTGGTATCTTGTGG	232					
Db	257	GAATTACTGTGTTGACATGCGGGCAACCAATTGACACAGTTGGTATCTTGTGG	308					
RESULT 11								
LOCUS	CA538859							
DEFINITION	CO272B01-5N N1A Mouse 7.5-dpc Whole Embryo cDNA Library (long) Mus							
ACCESSION	CA538859							
VERSION	CA538859.1	GI:25080828						
KEYWORDS	EST.							
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mus musculus							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
	1 (bases 1 to 503)							
	Pao, Y., Kargul, G.J., Dudenkula, D.B., Qian, Y., Tanaka, T., Lin, M.K.,							
	Luo, A. and Ko, M.S.H.							
	Systematic Analyses of N1A Mouse 7.5-dpc Whole Embryo cDNA Library							
	(long)							
	Unpublished (2001)							
	Other ESTs: CO272B01-3							
	Contact: Dawood B. Dudekula							
	Laboratory of Genetics							
	National Institute on Aging/National Institutes of Health							
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA							
	Email: cdna@igsun.gsc.nia.nih.gov							
	Phone: C0272 row: B column: 01							
	Seq. primer: M13 Reverse							
	High quality sequence stop: 503							
	POLYA=No.							
FEATURES								
source	location/Qualifiers							
	1..503							

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/cisise_type="Leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="RDH 08"

clone_jib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HSC project="TCBA"
/name="Vector: lambda psb; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'-GAGGAGCTCGAGCGCGGAGGAGG(T'VN
3'-) V=A,C,G; N=A,C,G,T) and then dg tailed. Second strand
was primed with a BamH1-dC primer
(5'-AGAGGCTCGGATCGCGCGCGCATATATATAT(C) 3'1.
Double-stranded cDNA was then digested with BamH1 and XhoI
and directionally cloned into the BamH1 and SalI sites of
lambda psb vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Garnini P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoaka S, Saekian, Okazaki Y, Muramatsu W,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper",
Natl Res 4: 1,61-6, Feb 28, 1997)".

```

Query Match	69.9%	Score 205.4	DB 4	Length 313
Best Local Similarity	92.7%	Pred. No. 3-46		
Matches 215; Conservative	0	Mismatches 17	Indels 0	Gaps 0

QY 1 ACATATGCGCGCCCTCATTTTGGACCAATTAGAGCTTCAGATTTTATGACTCT 60
 |||

QY 1 ACATATGGCGCTCCCAAGTTGACATAATTGGAAGCTGCAGATTTTATTCATCCT 60

separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal-I-S. The

Products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 69.5%; Score 204.4; DB 6; Length 503;
Best Local Similarity 81.0%; Pred. No. 6,8e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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DB 252 CAAGAGGATGGAAGAAATTAGCTAGCTATTAAAAACATCTGTGATATGATAC 311
QY 121 AATCAGTTCCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 180
DB 312 AATCAGTTCCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 371
QY 181 GAATTAAGTCTGTTGATGCGGCGACCAAAATTCAGATGTTGATCTTTTG 240
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RESULT 12

B0552228

LOCUS

DEFINITION H4014C09-5 N1A Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4014C09 5', mRNA sequence.

ACCESSION

B0552228

VERSION

B0552228.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 598)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,
Martin, P.R., Stagg, C.A., Basey, U., Aiba, K., Hamatani, T.,
Kargul, G.J., Luo, A.G., Kelso, J., Hide, W., and Ko, M.S.H.,
Assembly, verification, and initial annotation of N1A 7.4K mouse
cDNA clone set
Genome Res. 12 (12), 1999-2003 (2002)
22354164
12466305
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/N1A_7_4k.html for details.
Plate: H4014 row: C column: 09
Seq primer: -21M13 Reverse
High quality sequence stop: 598
POLYA=no.

FEATURES

source

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/clone_lib="N1A Mouse 7.4K cDNA Clone Set"
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clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN

Query Match 69.5%; Score 204.4; DB 5; Length 598;
Best Local Similarity 81.0%; Pred. No. 7e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 1 ACATATGCGCGCTGCTCAATCTTGAAGTCTGATTTATGATCT 60
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DB 356 GAACGCTGTTGATGCGGCGACCAAAATTCAGATGTTGATCTTTTG 415
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RESULT 13

BB660378

LOCUS

DEFINITION BB660378 RIKEN full-length enriched, 13 days embryo lung Mus
musculus cDNA clone D43042L21 5', mRNA sequence.

ACCESSION

BB660378

VERSION

BB660378.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 610)
Arai, K., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arai, K., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A.

and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, K.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
source

1. .610
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lung"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCGCACTGTTTCTTTTCTTTT 3']. cDNA was
transcribed using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGTTCTCGAGTTAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FHC I."

ORIGIN

Query Match 69.5%; Score 204.4; DB 2; Length 610;
Best Local Similarity 81.0%; Pred. No. 7e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
1 ACATATGCGGCTGCTCAATGTTGACCTAATTAGAGAGCTGTCAGATTATGATCT 60
212 ACATATGCGGCTGCTCAATGTTGACCTAATTAGAGAGCTGTCAGATTATGATCT 271
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332 AATGCTTCAATTAAGAGATTTGAGCATTACTTCAATGAGAAAAGTCCACTTCT 391
181 GAATATGTTTGAATGAGGAGCAACAATGTCAGATGTTGATCTTGATCTTTTG 240
392 GAATATGTTTGAATGAGGAGCAACAATGTCAGATGTTGATCTTGATCTTTTG 451
241 ATCCAAAATGATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCC 294
452 GTCCAGATGAGTCTTTGCCCCCGCACTCTCGTGGCGGAGCGGATCTTCC 505

RESULT 14
BB613447
LOCUS BB613447 637 bp mRNA linear EST 26-OCT-2001

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

BB613447 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732482P03 5', mRNA sequence.

BB613447.1 GI:16454055

EST.

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 637)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ichii, Y., Itoh, M., Kawai, J.,
Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanuki, M., Yoneda, Y., Ishikawa, T., Oawa, K., Tanaka, T.,
Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kikuta, A.
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, K.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
source

1. .637
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skin"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGTTCTCGAGTTAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence (5' GAGAGAGAGATTCGATTAATTAATTCACCCCCCCCC 3'). cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 69.5%; Score 204.4; DB 2; Length 637;
Best Local Similarity 81.0%; Pred. No. 7,1e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGTGGCGCTCCCTCAATGTGGAGCTAAATGAAAGCTGTCAGATTTATTGATCTT 60
DB 193 ACATACATACCGCAACCTTAATGTGGGGATCCTTAGGAAGCTGCGATTTATTGATCTT 252
QY 61 CAAAGAGATGGAGAGTGTAGTGTATTAATAAACAATCTGTGATGATGATGATAC 120
DB 253 CAAAGAGGTTGAGAGATTTAGAGTGTATTAATAAAGCCGTCGGGAGAGAGATAC 312
QY 121 AATCAGTTTCATAGAGATTTGAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 180
DB 313 AATCAGTTTCATATAGAGATTTGAGCATTTACTTCAAGCCGGAGAGAGCCCACTCT 372
QY 181 GAATTAAGTGTGAGTGGGAGCAACAATATGCAAGTGTGATCTTTGATCTTTTG 240
DB 373 GAATGCTGTTGAGTGGGAGCAACAATATGCAAGTGTGATCTTTGATCTTTG 432
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCCCAAGATGCTTTCC 294
DB 433 GTCCAGATGAGTGTGTTGTCCTCCCGCCCACTCTCTGCGAGATGCGTTCC 486

RESULT 15

BY721552 638 bp mRNA linear EST 17-DEC-2002
LOCUS BY721552 RIKEN full-length enriched, adult male diencephalon Mus
DEFINITION musculus cDNA clone 9330209D03 5', mRNA sequence.
BY721552
ACCESSION BY721552.1 GI:27134669
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oshio, K., Saito, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schirral, L. M., Kanapin, A., Matsuda, H., Batilov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Chotiba, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guethlich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochik, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sutarau, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Vitaranda, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. S., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

JOURNAL
MEDLINE
PUBMED
COMMENT

Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, R., Ohno, M., Ohnaka, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, W., Takeda, Y., Waki, K., Watanabe, A., Yamashita, M. and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
SOURCE

1. 638
/organism="Mus musculus"
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ORIGIN

Query Match 69.5%; Score 204.4; DB 6; Length 638;

Best Local Similarity 81.0%; Pred. No. 7.1e-46;

Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY     241 ATCCAAATGATTTTGTGCTCTGAGATCTTTTGTCCCAATGCTGTTCCC 294
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Job time : 1944 secs

PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX Claim 18; Page 173-174; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 DD cDNA

Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.4e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGTCGCGCTGCATGTTGACATTAATGAGAGCTGCAGATTTTATGATCT 60
 DB 1 AATATGTCGCGCTGCATGTTGACATTAATGAGAGCTGCAGATTTTATGATCT 60
 QY 61 CAAGAAGATGAGAAAGTTAGCTGTAGTATTAATAAACAATCTGGTGTATGATGAC 120
 DB 61 CAAGAAGATGAGAAAGTTAGCTGTAGTATTAATAAACAATCTGGTGTATGATGAC 120
 QY 121 AATCAGTTTCACATTAAGAGATTTGAAGCACTTAATCTCAAACTGGAAGATCCACTTC 180
 DB 121 AATCAGTTTCACATTAAGAGATTTGAAGCACTTAATCTCAAACTGGAAGATCCACTTC 180
 QY 181 GAATTAAGTGTGACGCGGACACCAAAATTTGACAGTTGGATCTTTTG 240
 DB 181 GAATTAAGTGTGACGCGGACACCAAAATTTGACAGTTGGATCTTTTG 240
 QY 241 ATCCAAATGAATTTTCTCTCGAGATCTTTTCTCCAGATCTGTCC 294
 DB 241 ATCCAAATGAATTTTCTCTCGAGATCTTTTCTCCAGATCTGTCC 294

RESULT 2

AADS5056
 ID AADS5056 standard; cDNA; 294 BP.

AC AADS5056;

DT 18-DEC-2003 (first entry)

DE Human IRAK4 DD cDNA.

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting death domain; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;

KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..294

FT /tag= a

FT /product= "Human IRAK4 DD protein"

FT /note= "No start and stop codon"

FT /partial

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

PA (REED/) REED J C.
 PA (GODZ/) GODZIK A.
 PA (PAWL/) PAWLOWSKI K.
 PA (PIOR/) FIORENTINO L.
 PA (LEES/) LEE S H.
 PA (ROTH/) ROTH W.
 PA (STEN/) STENNER-LIEWEN F.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liewen F;

DR WPI; 2002-500222/53.
 DR P-PSDB; AAB38897.

PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

Claim 18; Page 33-34; 99pp; English.

CC The present invention provides novel death domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDD) DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DDEs and NB-ARC
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 DD cDNA

Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.4e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCAATGTTGACTAATAGGAAGTGTGAGATTTTATGATCCT 60
 DB 1 ACATATGCGCTGCTCAATGTTGACTAATAGGAAGTGTGAGATTTTATGATCCT 60
 QY 61 CAAGAGAGATGGAAGATTGCTGTGACTATTAATAAACCATCTGTGTGATGATATAC 120
 DB 61 CAAGAGAGATGGAAGATTGCTGTGACTATTAATAAACCATCTGTGTGATGATATAC 120
 QY 121 AATAGTTTCACTAAGAGATTGAGCATTAATGAGAAAAGTCCACTTCT 180
 DB 121 AATAGTTTCACTAAGAGATTGAGCATTAATGAGAAAAGTCCACTTCT 180
 QY 181 GAATTACTGTTGACTGGGACCAACAATTGACAGTTGTGATCTTGTGATCTTTTG 240
 DB 181 GAATTACTGTTGACTGGGACCAACAATTGACAGTTGTGATCTTGTGATCTTTTG 240
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 294
 DB 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 294

RESULT 3

AAA09319
 ID AAA09319 standard; DNA; 833 BP.

AAA09319;

10-AUG-2000 (first entry)

Human cancer associated antigen precursor DNA, clone NY-REN-64.

renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;

88.

Homo sapiens.

Location/Qualifiers

Key 50..670

PT CDS

FT

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 3; Length 833;

Best Local Similarity 100.0%; Pred. No. 1.9e-77;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCAATGTTGACTAATAGGAAGTGTGAGATTTTATGATCCT 60
 DB 74 ACATATGCGCTGCTCAATGTTGACTAATAGGAAGTGTGAGATTTTATGATCCT 133
 QY 61 CAAGAGAGATGGAAGATTGCTGTGACTATTAATAAACCATCTGTGTGATGATATAC 120
 DB 134 CAAGAGAGATGGAAGATTGCTGTGACTATTAATAAACCATCTGTGTGATGATATAC 193
 QY 121 AATAGTTTCACTAAGAGATTGAGCATTAATGAGAAAAGTCCACTTCT 180
 DB 194 AATAGTTTCACTAAGAGATTGAGCATTAATGAGAAAAGTCCACTTCT 253
 QY 181 GAATTACTGTTGACTGGGACCAACAATTGACAGTTGTGATCTTGTGATCTTTTG 240
 DB 254 GAATTACTGTTGACTGGGACCAACAATTGACAGTTGTGATCTTGTGATCTTTTG 313
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 294
 DB 314 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 367

RESULT 4

AAD40079
 ID AAD40079 standard; DNA; 1383 BP.

AAD40079;

22-OCT-2002 (first entry)

Human IRAK4 gene #1.

Human; death domain; DD; death effector domain; DED; Chlamydia infection;

NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;

inflammation; allergy; autoimmunity; allograft rejection; cell division;

immune-based pathology; fibrosis; arthritis; graft versus host disease;

immunosuppressive; gene therapy; antisense therapy; gene; ds.

Homo sapiens.

Location/Qualifiers

Key 1..1383

PT CDS

FT

XX

XX

XX

XX

XX

XX

XX

XX

XX

Obata Y, Gout I, Tureci O, Sahin U, Pfeundschuh M, Scanlan MJ;

Stocker E, Chen Y, Old LJ, Jager E, Knuth A;

WPI; 2000-303774/26.

P-PSDB; AAY92347.

Preventing, diagnosing and/or treating disorders associated with abnormal

expression of human cancer associated antigens.

Claim 57; Page 85; 121pp; English.

AA09310-20 are novel genes isolated by SEREX screening from a renal

cancer cell line 1973/10.4. The genes encode cancer associated antigen

precursors. These gene products are useful in methods for preventing,

diagnosing and/or treating disorders, especially cancer, associated with

abnormal expression of human cancer associated antigens. The method

comprises contacting a sample from a subject with an agent that

specifically binds to the nucleic acid molecule or expression product (or

fragment) complexed with a human leukocyte antigen (HLA) molecule and

determining the interaction between the agent and the nucleic acid

molecule or the expression product as a determination of the disorder

Claim 19; Page 180-182; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection, cell apoptosis, cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of *C. trachomatis*, *C.*
 CC muridarum, *C. pneumoniae*, and *C. psittaci* or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 gene
 XX
 SQ Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATATGCGCTGCTCAATGTTGACATTAATGAGAGCTGCAGATTATTTATGATCTT 60
 DB 25 ACAATATGCGCTGCTCAATGTTGACATTAATGAGAGCTGCAGATTATTTATGATCTT 84
 QY 61 CAAGAAGATGAGAGAGTGTAGCTGTATTAATTAATCAATCTGGTGTATGATATAC 120
 DB 85 CAAGAAGATGAGAGAGTGTAGCTGTATTAATTAATCAATCTGGTGTATGATATAC 144
 QY 121 AATCAGTTTACATTAAGAGATTGAAAGCTTACTCAAACTGGAAGATCCACCTTCT 180
 DB 145 AATCAGTTTACATTAAGAGATTGAAAGCTTACTCAAACTGGAAGATCCACCTTCT 204
 QY 181 GAATTAATGTTGATGCTGGGCGACCAAAATGTCAGATTGATCTTGTGATCTTTTG 240
 DB 205 GAATTAATGTTGATGCTGGGCGACCAAAATGTCAGATTGATCTTGTGATCTTTTG 264
 QY 241 ATCCAAATGAAATTTTCTCTCGGAGATCTTTGCTCCGAGATGCTTCC 294
 DB 265 ATCCAAATGAAATTTTCTCTCGGAGATCTTTGCTCCGAGATGCTTCC 318

RESULT 5
 AAD59061
 ID AAD59061 standard; cDNA; 1383 BP.
 XX
 AC AAD59061;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human IRAK4 full length gene #1.
 XX

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting death domain; cell adhesion;
 KW vasotrophic; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress responses; benign prostatic hypertrophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..1383
 FT /*tag= a
 FT /product= "Human IRAK4 protein"

US2003049702-A1.

PD 13-MAR-2003.

PF 15-NOV-2001; 2001US-00001254.

PR 17-NOV-2000; 2000US-00715893.

PR 17-NOV-2000; 2000US-0367360P.

PR 29-JUN-2001; 2001US-0301889P.

PA (REED/) REED J C.

PA (GODZIK/) GODZIK A.

PA (PAML/) PAWLOWSKI K.

PA (FIOR/) FIORENTINO L.

PA (LEES/) LEE S H.

PA (ROTH/) ROTH W.

PA (STEN/) STENNER-LIEWEN F.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PI Stenner-Liewen F;

DR WPI, 2002-500222/53.

DR P-PDB; AAB38902.

PT New polypeptide comprising a death domain or death effector domain,

PT useful for discovery of drugs that suppress infection, inflammation,

PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 19; Fig 10A, 99p; English.

XX The present invention provides novel death Domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDD) DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DEDs and NB-ARC
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
 XX

SQ Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAATATGCGCTGCTCAATGTTGACATTAATGAGAGCTGCAGATTATTTATGATCTT 60
 DB 25 ACAATATGCGCTGCTCAATGTTGACATTAATGAGAGCTGCAGATTATTTATGATCTT 84
 QY 61 CAAGAAGATGAGAGAGTGTAGCTGTATTAATTAATCAATCTGGTGTATGATATAC 120

Db 85 CAAGAAGATGAGAAAGTTAGCTGTAGCTATTAAAAAACCTGCTGATGATAGATAC 144
 Qy 121 AATCAGTTTCACATAGAGAGATTGAAAGCATTTACTTCAAACTGAGAAAAGTCCACTTCT 180
 Db 145 AATAGATTTCACATAGAGAGATTGAAAGCATTTACTTCAAACTGAGAAAAGTCCACTTCT 204
 Qy 181 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 240
 Db 205 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 264
 Qy 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 Db 265 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 318

RESULT 6

AAS76805 standard; cDNA; 1668 BP.
 XX AAS76805;

AC AAS76805;
 XX 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12609.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX P-PSDB; ABG12618.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 1; SEQ ID NO 12609; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS6197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 294; DB 5; Length 1668;

XX Best Local Similarity 100.0%; Pred. No. 2,4e-77;

XX Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGTGGCGCCCTCAATGTTTGAAGTAAATAGAAAGCTGCAGATTTTATGATCCT 60
 Db 25 ACATATGTGGCGCCCTCAATGTTTGAAGTAAATAGAAAGCTGCAGATTTTATGATCCT 84
 Qy 61 CAAGAAGATGAGAAAGTTAGCTGTAGCTATTAAAAACATCTGTGATGATAGATAC 120
 Db 85 CAAGAAGATGAGAAAGTTAGCTGTAGCTATTAAAAACATCTGTGATGATAGATAC 144
 Qy 121 AATCAGTTTCACATAGAGAGATTGAAAGCATTTACTTCAAACTGAGAAAAGTCCACTTCT 180
 Db 145 AATCAGTTTCACATAGAGAGATTGAAAGCATTTACTTCAAACTGAGAAAAGTCCACTTCT 204
 Qy 181 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 240
 Db 205 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 264
 Qy 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 Db 265 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 318

RESULT 7

AAD40085 standard; DNA; 2817 BP.
 ID AAD40085

XX AAD40085;

XX 22-OCT-2002 (first entry)

XX Human IRAK4 gene #2.

KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 50..1432
 FT /*tag= a
 FT /product= "Human IRAK4"

XX WO200240680-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001WO-US044844.

XX 17-NOV-2000; 2000US-00715893.

XX 29-JUN-2001; 2001US-0301889P.

XX (BURN-) BURNHAM INST.

XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

XX Steiner-Jewen F;

XX WPI: 2002-500222/53.

XX P-PSDB; AAE24865.

XX New polypeptide comprising a death domain or death effector domain,
 XX useful for discovery of drugs that suppress infection, inflammation,
 XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 19; Page 194-196; 2099p; English.

XX The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a protein or a drug
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent, and
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDD DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 gene
XX

SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 2.9e-77;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCT 60
DB 74 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCT 133
QY 61 CAAGAAGATGGAAGAGTTAGCTGTATTTAAACCATCTGGTATGATAGATAC 120
DB 134 CAAGAAGATGGAAGAGTTAGCTGTATTTAAACCATCTGGTATGATAGATAC 193
QY 121 AATCAGTTTCACTAAGAGATTTGAAGATTTCTCAAACTGGAAGAAAGTCCACTTCT 180
DB 194 AATCAGTTTCACTAAGAGATTTGAAGATTTCTCAAACTGGAAGAAAGTCCACTTCT 253
QY 181 GAATTAAGTGTGGAGTGGGACCAACAATGACAGTTGATCTTGATCTTTTG 240
DB 254 GAATTAAGTGTGGAGTGGGACCAACAATGACAGTTGATCTTGATCTTTTG 313
QY 241 ATCCAAATGAAATTTTGTCTCTGAGATCTTTTCTCCAGATCTGTTCCC 294
DB 314 ATCCAAATGAAATTTTGTCTCTGAGATCTTTTCTCCAGATCTGTTCCC 367

RESULT 8
AADS9067
ID AADS9067 standard; cDNA; 2817 BP.
XX
AC AADS9067;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human IRAK4 full length gene #2.
XX

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neuronal growth factor receptor-interacting death domain; cell adhesion;
KW vasotrophic; microbial infection; inflammation; allograft rejection; CTDD;
KW cell stress response; benign prostatic hypertrophy; antidiabetic; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;

KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..1432
FT /tag=a
FT /product="Human IRAK4 protein"
XX
XX US2003049702-A1.
XX
XX 13-MAR-2003.
XX
XX 15-NOV-2001; 2001US-00001254.
XX
XX 17-NOV-2000; 2000US-00715893.
XX 17-NOV-2000; 2000US-0367360P.
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (REED/) REED J C.
XX (GODZIK/) GODZIK A.
XX (PAWL/) PAWLOWSKI K.
XX (FIOR/) FIORENTINO L.
XX (LEES/) LEE S H.
XX (ROTH/) ROTH W.
XX (STEN/) STENNER-LIEWEN F.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
XX Stenner-Liewen F;
XX WPI; 2002-500222/53.
XX P-PSDB; AAE38908.
XX
XX New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 18; Page 51-53; 999p; English.

CC The present invention provides novel death Domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neuronal growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DEDs and NB-ARC
CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
XX

SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 2.9e-77;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCT 60
DB 74 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCT 133

CC (GenBank accession number NM_016123)
 XX Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 294; DB 10; Length 2817;
 Best Local Similarity 100.0%; Pred. No. 2,3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACATATGCGCCCTGCTCAATGTTGGACTAATTTAGGAAGCTGTGAGATTTATGATCCT 60
 Db ACATATGCGCCCTGCTCAATGTTGGACTAATTTAGGAAGCTGTGAGATTTATGATCCT 133

Qy 61 CAAGAGAGTGAAGAAAGTTAGCTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 120
 Db 134 CAAGAGAGTGAAGAAAGTTAGCTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 193

Qy 121 AATCAGTTTCACATPAAGAGATTGAGATTGAACTGTTGCTCCAGATGCTTTCC 180
 Db 194 AATCAGTTTCACATPAAGAGATTGAGATTGAACTGTTGCTCCAGATGCTTTCC 253

Qy 181 GAATTACTGTTTGAATGGGGGACCAAAATTGSCAGTTGGTGTGATCTTTG 240
 Db 254 GAATTACTGTTTGAATGGGGGACCAAAATTGSCAGTTGGTGTGATCTTTG 313

Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTTTCC 294
 Db 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTTTCC 367

RESULT 9
 ACC47548
 ID ACC47548 standard; DNA; 2817 BP.
 XX
 AC ACC47548;
 DT 11-JUL-2003 (first entry)
 XX
 DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.
 XX
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 50..1432
 FT /*tag= a
 FT /product= "IL-1 receptor-associated kinase-4"
 XX
 DE WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PE 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Freier SM;
 XX
 DR WPI; 2003-363256/34.
 DR P-PsDB; ABR44401.
 XX
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX
 PS Example 13; Page 80-83; 119pp; English.
 XX
 CC The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or
 CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence
 CC represents the human IL-1 receptor-associated kinase-4 encoding sequence

CC (GenBank accession number NM_016123)
 XX Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 294; DB 10; Length 2817;
 Best Local Similarity 100.0%; Pred. No. 2,3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACATATGCGCCCTGCTCAATGTTGGACTAATTTAGGAAGCTGTGAGATTTATGATCCT 60
 Db ACATATGCGCCCTGCTCAATGTTGGACTAATTTAGGAAGCTGTGAGATTTATGATCCT 133

Qy 61 CAAGAGAGTGAAGAAAGTTAGCTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 120
 Db 134 CAAGAGAGTGAAGAAAGTTAGCTGTAGCTATTAAAAAACCATCTGTGATGATGATAC 193

Qy 121 AATCAGTTTCACATPAAGAGATTGAGATTGAACTGTTGCTCCAGATGCTTTCC 180
 Db 194 AATCAGTTTCACATPAAGAGATTGAGATTGAACTGTTGCTCCAGATGCTTTCC 253

Qy 181 GAATTACTGTTTGAATGGGGGACCAAAATTGSCAGTTGGTGTGATCTTTG 240
 Db 254 GAATTACTGTTTGAATGGGGGACCAAAATTGSCAGTTGGTGTGATCTTTG 313

Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTTTCC 294
 Db 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTTTCC 367

RESULT 10
 AAD10197
 ID AAD10197 standard; cDNA; 1383 BP.
 XX
 AC AAD10197;
 DT 24-SEP-2001 (first entry)
 XX
 DE Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
 XX
 KW Human, interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic;
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1383
 FT /*tag= a
 FT /product= "Human IRAK-4"
 XX
 DE WO200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PR 12-JAN-2001; 2001WO-US001171.
 XX
 PR 13-JAN-2000; 2000US-0176395P.
 XX
 PA (TULDA-) TULARIX INC.
 XX
 PI Wesche H, Li S;
 XX
 DR WPI; 2001-451860/48.
 DR P-PsDB; AAB05398.

XX Novel human interleukin-1 receptor associated kinase polypeptide, useful
PT for identifying modulators of the polypeptide for treating gout, asthma,
PT allergic rhinitis, multiple sclerosis and skin cancer.
PT

PS Claim 7; Fig 2; 89pp; English.

The pretranscription sequence is a cDNA encoding human interleukin (IL)-1 receptor associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)- κ B activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumour, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, sarcoidosis and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NF κ B in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy.

SQ Sequence 1383 BP; 463 A; 244 C; 283 G; 393 T; 0 U; 0 Other;

Query Match	99.5%	Score 292.4;	DB 5;	Length 1383;
Best Local Similarity	99.7%	Pred. No. 6.9e-77;		
Matches 293; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	AACATATGAGGGCTGGCGCTCAAACTGTGACATTAATTAGAAAGCTGTGACAGATTATTATGATCCT	60
Db	25	AACATATGAGGGCTGGCGCTCAATGTGTGACATTAATTAGAAAGCTGTGACAGATTATTATGATCCT	84
QY	61	CAGAAGAGATGSAAGAGAGTTAGCTGTAGCTATTAAAAAACCATCTGGATGATGATAGTATAC	120
Db	85	CAGAAGAGATGSAAGAGAGTTAGCTGTAGCTATTAAAAAACCATCTGGATGATGATAGTATAC	144
QY	121	AATGAGTTTCACATTAAGAGAGATTGACATTAATTCTTCAAACTGSAAAAAGTCCCATCTCT	180
Db	145	AATGAGTTTCACATTAAGAGAGATTGAAACATTACTTCAAACTGSAAAAAGTCCCATCTCT	204
QY	181	GAATTAAGTGTGACTGCGGGACCAACAATAGCAACAGTGGTGATCTTGAGATCTTTGG	240
Db	205	GAATTAAGTGTGACTGCGGGACCAACAATAGCAACAGTGGTGATCTTGAGATCTTTGG	264
QY	241	ATCCAAATGSAATTTTTTGTCTCTCTCCAGACTTTTGTCTCCCAAGTGTGTTTCCC	294
Db	265	ATCCAAATGSAATTTTTTGTCTCTCTCCAGACTTTTGTCTCCCAAGTGTGTTTCCC	318

RESULT 11

ID AAS61608 standard; cDNA; 501 BP.

AA561608;

29-JAN-2002 (first entry)

Lung small cell carcinoma antigen, cDNA #149.

KM	Human; cytosol; carcinoma; lung small cell cancer antigen; tumour
KM	lung cancer; ss.
XX	
OS	
XX	Homo sapiens.
XX	
PN	WC200177168-A2.

PN WO200177168-A2

PD 18-OCT-2001.

PF 11-APR-2001; 2001WO-US011859.
XX

PR 11-APR-2000; 2000US-0196780P.

PR 01-SEP-2000; 2000US-0229763P.
DE 01-SEP-2000 0000Z
DD 01-SEP-2000 0000Z

PR 14-SEP-2000; 2000US-0232565P.
DB 19-DEC-2000; 2000US-0232565P.

PR 08-JAN-2001; 2001US-0260796P.
YY

PA (CORI-) CORIXA CORP.
XX

PI Lodes MJ, Wang T, Mohamath
XX

DR WPI; 2002-010896/01.
XX

PT Lung tumor polynucleotide and
PT diagnosis of cancer associated

XX
PS Claim 1: Page 174: 295m: End

XX The invention relates to novel
CC

cc polynucleotides (I) and polyp
cc cancer in a patient. The meth

oligonucleotides (III), where the biological sample from the patient is contacted with (II), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer specifically lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. A561460-A561874 represent novel human lung small cell cancer antigen coding sequences of the invention

SQ Sequence 501 BP; 166 A; 102 C; 97 G; 134 T; 0 U; 2 Other;

Query Match	82.2%	Score 241.6;	DB 6;	Length 501;
Best Local Similarity	97.3%	Pred. No. 7e-62;		
Matches 288; Conservative	0;	Mismatches 4;	Indels 4;	Gaps 4

[illegible]

QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 120
 |||||
 Db 105 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 164

121 AACCTAGSIIICACATAGAGAGTTTGAGCATTACTTCACAACTGGAAAAAGTCCACATTC 179
165 AATCAAGTTTACATAGAGAGTTTGAGCATTTCTCAAACTGGAAAAAGTCCACATTC 223

224 TTGATACGTTTGACTGGGGGCACCAAAATTGACAGTGGTGATCTTGCGATCTTT 283

284 TGAICCAAAATGAA TTTTGTCTCTGCAGCTTTTGTCTCCAGATGCTGTTCCC 338

RESULT 12
 AAD10198 standard; cDNA, 1542 BP.
 ID AAD10198
 AC AAD10198;
 XX
 XX
 24-SEP-2001 (first entry)
 DT
 XX
 DE Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
 XX
 XX Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; ss.
 KW
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1542
 FT /*tag= a
 FT /product= "Mouse IRAK-4"
 FT
 XX
 XX MO200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PD 12-JAN-2001; 2001MO-US001171.
 XX
 PP 13-JAN-2000; 2000US-0176395P.
 XX
 PR
 XX (TULIA-) TULARIK INC.
 PA
 XX Weesche H, Li S;
 PI
 XX WPI: 2001-451860/48.
 DR P-PSDB; AAB05399.
 XX
 PT Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Claim 26; Fig 4; 89pp; English.
 XX
 XX The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor
 CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and
 CC other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction

CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy
 XX
 SQ Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;
 Query Match 69.5%; Score 204.4; DB 5; Length 1542;
 Best Local Similarity 81.0%; Pred. No. 1.3e-50;
 Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 QY 1 ACATATGCGCGCTGCTCAATGTTGACTAATTAGAGAGCTGACATTATGATGCT 60
 DB 187 ACATACATACCGCAACCTTAATGTTGGATCCTTGGAGAGCTGTGGATTATGATCT 246
 QY 61 CAAGAAGGATGGAAGATTAGCTGTAGCTATTAAACCATCTGTGATGATATAC 120
 DB 247 CAAGAAGGATGGAAGATTAGCTGTAGCTATTCAAAAAGCGTCCGGGACAGACATAC 306
 QY 121 AATCAGTTTCAATTAAGGAGATTGAAAGCATTTACTTCAAACTGAAAAAGTCCACTCT 180
 DB 307 AATCAGTTTCAATTAAGGAGATTGAAAGCATTTACTTCAAACTGAAAAAGTCCACTCT 366
 QY 181 GAATTAATGTTGATGAGGACCAACCAATTCACAGTTGATGATGATGATTTTG 240
 DB 367 GAATGCTGTTGATGAGGACCAACCAATTCACAGTTGATGATGATGATTTTG 426
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 294
 DB 427 GTCCGATTGAGCTGTTGCTCCCGCACTCTCTGCTGCGGATGCCGTTCC 480
 RESULT 13
 ACC47549
 ID ACC47549 standard; DNA, 31000 BP.
 XX
 XX ACC47549;
 AC
 XX
 DT 11-JUL-2003 (first entry)
 XX
 DE Human DNA complement sequence # SEQ ID 10.
 XX
 XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Freier SM;
 XX
 DR WPI: 2003-363256/34.
 XX
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX
 PS Example 15; Page 85-102; 119pp; English.

XX The invention relates to a compound of 8-50 nucleobases which is targeted
CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
CC kinase-4, specifically hybridising with the nucleic acid and inhibiting
CC the expression of the encoded product. Also disclosed is the compound
CC hybridising with an 8-nucleobase portion of an active site on a nucleic
CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
CC oligonucleotide is useful for treating an animal having a disease or
CC (particularly renal cancer), inflammatory disease or an infection. The
CC antisense compounds are useful for diagnostics, therapeutics,
CC prophylaxis or as research reagents or kits. The current sequence is
CC utilised in an example from the invention in the design of antisense
CC oligonucleotides, and represents the complement of the human DNA sequence
CC that is given as GenBank accession number AC016143
XX

SQ Sequence 31000 BP; 9247 A; 5856 C; 5924 G; 9973 T; 0 U; 0 Other;

Query Match 51.6%; Score 151.8; DB 10; Length 31000;
Best Local Similarity 95.7%; Pred. No. 1.7e-34;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCACTTTCACATAGAGAGATTGAAGCATTTCAACTGGAAGAAAGTCCCACTTGTGA 182
DB 12953 TTAATTACTTTTAAGAGATTGAAGCATTTCAACTGGAAGAAAGTCCCACTTGTGA 13012
QY 183 ATTACTGTTGACTGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTTGAT 242
DB 13013 ATTACTGTTGACTGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTCTGAGTCTTTGTCTCCAGAT 285
DB 13073 CCAAAATGAATTTTGTCTCTGAGTCTTTGTCTCCAGAT 13115

RESULT 14
ID AAS76803
AA576803 standard; cDNA; 405 BP.

AC AAS76803;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12607.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HSE-) HSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG12616.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 1; SEQ ID NO 12607; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC Sequences. (I) is useful as hybridisation probe, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;

Query Match 51.2%; Score 150.4; DB 5; Length 405;
Best Local Similarity 99.3%; Pred. No. 1e-34; 1; Indels 0; Gaps 0;
Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 TAAGAGATTGAAGCATTTCAACTGGAAGAAAGTCCCACTTGTGATCTTTTG 193
DB 115 TAAGAGATTGAAGCATTTCAACTGGAAGAAAGTCCCACTTGTGATCTTTTG 174
QY 194 ACTGGGGACCAAAATTGACAGTTGGATCTTGGATCTTTGATCCAAATGAAT 253
DB 175 ACTGGGGACCAAAATTGACAGTTGGATCTTGGATCTTTGATCCAAATGAAT 234
QY 254 TTTTGTCTCTGCGAGTCTTTGTCTCCAGAT 285
DB 235 TTTTGTCTCTGCGAGTCTTTGTCTCCAGAT 266

RESULT 15
ID AAD40084
AAD40084 standard; DNA; 211 BP.

AC AAD40084;

DT 22-OCT-2002 (first entry)

DE Human IRAK4 short gene.

KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW immunosuppressive; gene therapy; antisense therapy; gene; ds.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..180

FT /tag= a

FT /product= "Human IRAK4 short protein"

PN WO200240680-A2.

PD 23-MAY-2002.

PF 15-NOV-2001; 2001WO-US044844.

PR 17-NOV-2000; 2000US-00715893.

PR 29-JUN-2001; 2001US-0301889P.

PA (BURN-) BURNHAM INST.

XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Stemmer-Liwen F,

XX WPI; 2002-500222/53.
DR P-PSDB; AAE24864.

XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX
PS Claim 19; Page 195; 209pp; English.

XX
CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDD DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 short gene
XX

XX
SQ Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;

Query Match 46.8%; Score 137.6; DB 6; Length 211;

Best Local Similarity 97.2%; Pred. No. 5.5e-31;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
|||

DB 25 ACATATGCGCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 84
|||

QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAAACCATCTGTGTGATGATGATAC 120
|||

DB 85 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAAACCATCTGTGTGATGATGATAC 144
|||

QY 121 AATCAGTTTCACATTAAGAGATT 144
|||

DB 145 AATCAGTTTCACATTAAGAGATT 168
|||

Search completed: January 12, 2005, 04:35:56
Job time: 321 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:29:43 ; Search time 1843 Seconds
(without alignments)
7543.772 Million cell updates/sec

Title: US-10-001-254-5
Perfect score: 294
Sequence: 1 acatattgtgcgtcgtcctca.....tgcctccagatcgtctccc 294

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	100.0	294	6	AX431296 Sequence
2	294	100.0	833	6	AR223870 Sequence
3	294	100.0	1383	6	AX431306 Sequence
4	294	100.0	1636	9	AY340962 Homo sapi
5	294	100.0	1684	9	AY340963 Homo sapi
6	294	100.0	2775	6	CQ728380 Sequence
7	294	100.0	2817	6	AR475548 Sequence
8	294	100.0	2817	6	AX431318 Sequence
9	294	100.0	2817	9	AF155118 Homo sapi
10	294	100.0	2820	9	AK000528 Homo sapi
11	292.4	99.5	1381	9	AY283671 Homo sapi
12	292.4	99.5	1383	6	AX196260 Sequence
13	292.4	99.5	1383	9	AF445802 Homo sapi
14	292.4	99.5	1383	9	AY283670 Homo sapi
15	292.4	99.5	1629	9	BC013316 Homo sapi
16	241.6	82.2	501	6	AX321132 Sequence
17	217	73.8	1703	9	AY340966 Homo sapi
18	217	73.8	1751	9	AY340967 Homo sapi
19	204.4	69.5	1542	6	AX196262 Sequence

20	204.4	69.5	1542	10	AF445803	AF445803 Mus muscu
21	204.4	69.5	2431	10	BC051676	BC051676 Mus muscu
22	151.8	51.6	31000	6	AR475555	AR475555 Sequence
23	151.8	51.6	33033	9	AY186092	AY186092 Homo sapi
24	151.8	51.6	118572	9	AC093012	AC093012 Homo sapi
25	151.8	51.6	165868	2	AC021719	AC021719 Homo sapi
26	151.8	51.6	309582	2	AC025567	AC025567 Homo sapi
27	137.6	46.8	211	6	AX431316	AX431316 Sequence
28	137.6	46.8	470	6	CO681170	CO681170 Sequence
29	137.6	46.8	1490	9	AY340964	AY340964 Homo sapi
30	137.6	46.8	1538	9	AY340965	AY340965 Homo sapi
31	137.6	46.8	1781	9	AK027301	AK027301 Homo sapi
32	137.6	46.8	2213	6	AX875837	AX875837 Sequence
33	137.6	46.8	2213	6	BD155790	BD155790 Primer fo
34	110	37.4	264657	2	AC129390	AC129390 Rattus no
35	99.8	33.9	205374	10	AC147160	AC147160 Mus muscu
36	94.8	32.2	1452	5	AY616584	AY616584 Danto rer
37	94.8	32.2	1719	5	BC045381	BC045381 Danto rer
38	61.4	20.9	244696	2	AC123081	AC123081 Rattus no
39	61.4	20.9	252400	2	AC094859	AC094859 Rattus no
40	54.2	18.4	756	11	BV075713	BV075713 S212P604
41	46.8	15.9	88858	2	AC134788_3	Continuation (4 of
42	46.8	15.9	110000	2	AC103663_1	Continuation (2 of
43	43	14.6	9990	1	AE010646	AE010646 Fusobacte
44	42.8	14.6	574	11	BV034947	BV034947 S212P6037
45	42.6	14.5	1691	6	CQ719522	CQ719522 Sequence

ALIGNMENTS

RESULT 1
AX431296
LOCUS AX431296 294 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 5 from Patent WO0240680.
ACCESSION AX431296
VERSION AX431296.1 GI:21656165
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S. H., Reed, J. C.,
Roth, W. and Steneger-Liemen, F.
Novel death domain proteins
Patent: WO 0240680-A 5 23-MAY-2002;
BURNHAM INST (US)

TITLE
JOURNAL
BURNHAM INST (US)

FEATURES
source
location/Qualifiers
1..294
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/mol_type="unassigned DNA"
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/note="unnamed protein product"
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/db_xref="GI:21656166"
/translation="TTYRCLNVGLIRKLSDPFGKWLAAVAKKPSGDDRYNQFH
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CDS

ORIGIN
Query Match 100.0%; Score 294; DB 6; Length 294;
Best Local Similarity 100.0%; Pred. No. 2e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR
1 ACATATGTCGCTCCCTCAATGTTGACTAATAGGAAGTGTGAGATTATGATCCT 60
ATATGTCGCTCCCTCAATGTTGACTAATAGGAAGTGTGAGATTATGATCCT 60
DB 1 ACATATGTCGCTCCCTCAATGTTGACTAATAGGAAGTGTGAGATTATGATCCT 60
CAAGAAGATGGAAGAGATTAGCTGTGATTAATAAACCATCTGATGATGATATAC 120
61 CAAGAAGATGGAAGAGATTAGCTGTGATTAATAAACCATCTGATGATGATATAC 120

QY 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
 DB 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
 QY 181 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 240
 DB 181 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 240
 QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 294
 DB 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 294

RESULT 2
 LOCUS AR223870 833 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 10 from patent US 6440663.
 ACCESSION AR223870
 VERSION AR223870.1 GI:23332452
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 833)
 AUTHORS Scanlan,M.J., Stockert,E., Chen,Y.-T., Old,L.J., Jager,E. and Knuth,A.
 TITLE Renal cancer associated antigens and uses thereof
 JOURNAL Patent: US 6440663-A 10 27-AUG-2002;
 FEATURES
 source 1. 833
 Location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 294; DB 6; Length 833;
 Best Local Similarity 100.0%; Pred. No. 1.8e-64;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACTATGTCGCTGCTCAATGTTGACCTAATTAGGAAGCTGTCAATTTTATTTGATCTT 60
 DB 74 AACTATGTCGCTGCTCAATGTTGACCTAATTAGGAAGCTGTCAATTTTATTTGATCTT 133
 QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAACATCTGTGATGATATAC 120
 DB 134 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAACATCTGTGATGATATAC 193
 QY 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
 DB 194 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 253
 QY 181 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 240
 DB 254 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 313
 QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 294
 DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 367

RESULT 3
 LOCUS AX431306 1383 bp DNA linear PAT 28-JUN-2002
 DEFINITION Sequence 15 from Patent WO0240680.
 ACCESSION AX431306
 VERSION AX431306.1 GI:21656175
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 AUTHORS Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C.,

TITLE Roth,W. and Stenmer-Liwen,F.
 JOURNAL Novel death domain proteins
 BURNHAM INSR (US)
 source Location/Qualifiers
 1. 1383
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.7e-64;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACTATGTCGCTGCTCAATGTTGACCTAATTAGGAAGCTGTCAATTTTATTTGATCTT 60
 DB 25 AACTATGTCGCTGCTCAATGTTGACCTAATTAGGAAGCTGTCAATTTTATTTGATCTT 84
 QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAACATCTGTGATGATATAC 120
 DB 85 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAACATCTGTGATGATATAC 144
 QY 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
 DB 145 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTCT 204
 QY 181 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 240
 DB 205 GAATTAATCTGTTGACTGGGGGACCAACAATTGACAGATTGATCTTGTGGATCTTTTG 264
 QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 294
 DB 265 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTTCCC 318

RESULT 4
 LOCUS AY340962 1636 bp mRNA linear PRI 01-AUG-2004
 DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4)
 ACCESSION AY340962
 VERSION AY340962.1 GI:37727958
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1636)
 AUTHORS Chuang,T.H. and Ulevitch,R.J.
 TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1636)
 AUTHORS Chuang,T.H. and Ulevitch,R.J.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
 FEATURES
 source 1. 1636
 Location/Qualifiers

gene
CDS
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/chromosome="12"
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1. 1636
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66. 1448
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DNRNQHIRFEALDQTKSPISSELPFDWGTNCTVGLVDLILQNEFPAPSLLP
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VDITBELKQFPDQIKVMKCOHENVELGSSDGDLCIVYVNPNSLDRLSC
LDGTPUSMWRCKLAQGANGLFLENHHIRHDIKSANITLDEAFKATISDGLAR
ASEKFAQVTWTSRIVGTAYAPALGELTPKSDIYSFVLLIETGLPAVDENR
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ORIGIN

Query Match 100.0%; Score 294; DB 9; Length 1636;
Best Local Similarity 100.0%; Pred. No. 1.7e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGCGCGCCCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCCT 60
Db 90 ACATATGCGCGCCCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCCT 149
Qy 61 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTAAAAACATCTGCTGATGATGATAC 120
Db 150 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTAAAAACATCTGCTGATGATGATAC 209
Qy 121 AATGAGTTTCATPAGAGATTGGAAGCATTAATTGAAAAAGTCCCATCTCT 180
Db 210 AATGAGTTTCATPAGAGATTGGAAGCATTAATTGAAAAAGTCCCATCTCT 269
Qy 181 GAATTAAGTTTGAATGCGGACCACAAAATTCAGATGCTGATCTTTTGG 240
Db 270 GAATTAAGTTTGAATGCGGACCACAAAATTCAGATGCTGATCTTTTGG 329
Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCC 294
Db 330 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCC 383

RESULT 5
AY340963 1684 bp mRNA linear PRI 01-AUG-2004
LOCUS Homo sapiens interleukin-1 receptor-associated kinase 4 variant
DEFINITION (IRAK4) mRNA, complete cds, alternatively spliced.
ACCESSION AY340963
VERSION AY340963.1 GI:37727960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1684)
AUTHORS Chuang,T.H. and Ulevitch,R.J.
TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1684)
AUTHORS Chuang,T.H. and Ulevitch,R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
Location/Qualifiers

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114. 1496
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variant"
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ORIGIN

Query Match 100.0%; Score 294; DB 9; Length 1684;
Best Local Similarity 100.0%; Pred. No. 1.7e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATATGCGCGCCCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCCT 60
Db 138 ACATATGCGCGCCCTCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCCT 197
Qy 61 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTAAAAACATCTGCTGATGATGATAC 120
Db 198 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTAAAAACATCTGCTGATGATGATAC 257
Qy 121 AATGAGTTTCATPAGAGATTGGAAGCATTAATTGAAAAAGTCCCATCTCT 180
Db 258 AATGAGTTTCATPAGAGATTGGAAGCATTAATTGAAAAAGTCCCATCTCT 317.
Qy 181 GAATTAAGTTTGAATGCGGACCACAAAATTCAGATGCTGATCTTTTGG 240
Db 318 GAATTAAGTTTGAATGCGGACCACAAAATTCAGATGCTGATCTTTTGG 377
Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCC 294
Db 378 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCC 431

RESULT 6
CQ728380 2775 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 14314 from Patent WO02068579.
DEFINITION CQ728380
ACCESSION CQ728380
VERSION CQ728380.1 GI:42297030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
JOURNAL thereof
JOURNAL Patent: WO 02068579-A 14314 06-SEP-2002;
JOURNAL PB Corporation (NY) (US)
FEATURES
source 1. 2775
Location/Qualifiers

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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 294; DB 6; Length 2775;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 60
DB 36 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 95
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 120
DB 96 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 155
QY 121 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 180
DB 156 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 215
QY 181 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 240
DB 216 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 275
QY 241 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 294
DB 276 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 329

RESULT 7
AR475548 2817 bp DNA linear PAT 20-FEB-2004
LOCUS AR475548
DEFINITION Sequence 3 from patent US 6692959.
ACCESSION AR475548
VERSION AR475548.1 GI:42715031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2817)
AUTHORS Bennett,C.F. and Freier,S.M.
TITLES Antisense modulation of IL-1 receptor-associated kinase-4
expression
JOURNAL Patent: US 6692959-A 3 17-FEB-2004;
FEATURES
source
1.2817
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/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 60
DB 74 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 120
DB 134 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 193
QY 121 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 180
DB 194 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 253
QY 181 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 240
DB 254 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 294

DB 314 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 367

RESULT 8
AX431318 2817 bp DNA linear PAT 28-JUN-2002
LOCUS AX431318
DEFINITION Sequence 27 from Patent WO0240680.
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C.,
Roth,W. and Steiner-Jewen,F.
TITLES Novel death domain proteins
JOURNAL Patent: WO 0240680-A 27 23-MAY-2002;
BURNHAM INST (US)

FEATURES
source
1.2817
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/db_xref="taxon:9606"

CDS

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/db_xref="GI:21656188"
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ORIGIN

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 60
DB 74 ACATATGCGCGCTGCTCAATGTTGACTATTTGAAAGCTGTCAAGATTTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 120
DB 134 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTTAAAAACCATCTGGTATGATAGATAC 193
QY 121 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 180
DB 194 AATCAGTTTCACTAAGAGATTTGAGCATTTCAACTGGAAAAAGTCCACTTCT 253
QY 181 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 240
DB 254 GAATTAAGTGTGCTGGGCAACCAAAATTCACAGTGGTATCTTGGATCTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTCGAGTCTTTGTCCAGATGCTGTTCC 367

RESULT 9
AF155118 2817 bp mRNA linear PRI 05-JAN-2000
LOCUS AF155118
DEFINITION Homo sapiens putative protein kinase NY-REN-64 antigen mRNA,
complete cds.
ACCESSION AF155118
VERSION AF155118.1 GI:5360130

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Scamlen,M.J., Gordon,J.D., Williamson,B., Stockert,E., Bander,N.H., Jorgensen,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T., and Old,L.J.
TITLE Antigens recognized by autologous antibody in patients with renal-cell carcinoma
JOURNAL Int. J. Cancer 83 (4), 456-464 (1999)
MEDLINE 99438124
PUBMED 10508479
REFERENCE 2 (bases 1 to 2817)
AUTHORS Scamlen,M.J., Gordon,J.D., Williamson,B., Stockert,E., Bander,N.H., Jorgensen,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T., and Old,L.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
FEATURES
SOURCE Location/Qualifiers
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/cell_line="1973/10-4"
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/db_xref="GI:5360131"
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ORIGIN
Query Match 100.0%; Score 294; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACATATGCGCGCTGCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 60
DB 74 ACATATGCGCGCTGCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATATAC 120
DB 134 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATATAC 193
QY 121 AATGAGTTTCACATPAAGAGATTGAAGCATTTCTCAATCGAAAAAGTCCCATCT 180
DB 194 AATGAGTTTCACATPAAGAGATTGAAGCATTTCTCAATCGAAAAAGTCCCATCT 253
QY 181 GAATTAAGTTGAGTGGGACCACAAAATGTCACAGTGTGATCTTGTGATCTTTG 240
DB 254 GAATTAAGTTGAGTGGGACCACAAAATGTCACAGTGTGATCTTGTGATCTTTG 313
QY 241 ATCAAAATGAATTTTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 294
DB 314 ATCAAAATGAATTTTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTTTCC 367

RESULT 10
AK000528 2820 bp mRNA linear PRI 13-SEP-2003
LOCUS AK000528
DEFINITION Homo sapiens cDNA FLJ20521 f18, clone KAT10395.

ACCESSION AK000528
VERSION AK000528.1 GI:7020683
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H., Ota,T., Suzuki,Y., Okeyashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isega,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2820)
Sugano,S., Suzuki,Y., Ota,T., Okeyashi,M., Nishi,T., Isega,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Department of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: f18cna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
FEATURES
SOURCE Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10395"
/cell_line="KATO III"
/cell_type="signet-ring cell carcinoma"
/clone_id="KAT"
/note="Cloning vector pME18SF13"
30..1412
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ORIGIN
Query Match 100.0%; Score 294; DB 9; Length 2820;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACATATGCGCGCTGCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 60
DB 54 ACATATGCGCGCTGCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 113
QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATATAC 120
DB 114 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATATAC 173
QY 121 AATGAGTTTCACATPAAGAGATTGAAGCATTTCTCAATCGAAAAAGTCCCATCT 180
DB 174 AATGAGTTTCACATPAAGAGATTGAAGCATTTCTCAATCGAAAAAGTCCCATCT 233
QY 181 GAATTAAGTTGAGTGGGACCACAAAATGTCACAGTGTGATCTTGTGATCTTTG 240
DB 234 GAATTAAGTTGAGTGGGACCACAAAATGTCACAGTGTGATCTTGTGATCTTTG 293

OY 241 ATCAAATGTAATTCTTGTCCGGAGTTTGTCACCAATGCTGTCCC 294
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Db 294 ATCAAATGAATTCTCGCAGACTTTTGCCTCCAAGTCGTGCC 347

RESULT 11	AY283671	1381 bp	mRNA	linear	PRI 17-TUN-2003
LOCUS	AY283671				
DEFINITION	Homo sapiens interleukin-1 receptor associated kinase 4 mutant form				
ACCESSION	AY283671				
VERSION	AY283671.1	GI:31871819			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 1381)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
Salkowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N.
Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to

J. Exp. Med. (2003) In press

Meuevnev, A.E., Denisov, A., Kunits, D.B., Branco, J.C.G., Salkowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N.

JOURNAL
Submitted (25-APR-2003) Microbiology and Immunology, University of
Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD
21201-1559, USA

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source      Location/Qualifiers
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/ gene="IRAK4"
1. .657
CDS

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/product="interleukin-1 receptor associated kinase 4
mutant form 2"
/protein_id="AAP57090.1"
/db_xref="GI:31871820"
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619^620
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Accession Number AY283670 and wild-type IRAK4"
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variation

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Query Match	99.5%	Score 292.4;	DB 9;	Length 1381;
Best Local Similarity	99.7%	Pred. No. 4.3e-64;		
Matches 293; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	Db	QY
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25	ACATATATGCGCCTGCTCAATGTTGGACCTAATTAGGAAGCTGTCAGATTTTATGATCTT	84
61	CAAGAGGAGTGGAGGAAGTTAGCTGTAGCTCTTTAAAAAACCATCTGGTGATGATGATAC	120
85	CAAGAGGAGTGGAGGAAGTTAGCTGTAGCTCTTTAAAAAACCATCTGGTGATGATGATAC	144

QY 121 AATCAGTTTACATAGAGAAATTTGAAGCATTTACTTCAAACCTGAGAAAAGTCCACTTCT 180
 Db 145 AATCAGTTTACATAGAGAAATTTGAAGCATTTACTTCAAACCTGAGAAAAGTCCACTTCT 204

QY 181 GAATTACTGTTTGA CTGGGGCACCA CAAATTGCACAGTTGGTGCATTTGTGGATCTTTTG 240
|||
Db 205 GAATTACTGTTTGA CTGGGGCACCA CAAATTGCACAGCTGGTGCATTTGTGGATCTTTTG 264
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QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCCC 294
Ddb 265 ATCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCCC 318

RESULT 12
AX196260

LOCUS	1383 bp	DNA	linear	PAT 28-AUG-2001
AX196260				
DEFINITION	Sequence 2 from Patent WO0151641.			
SEQUENCE	sequence			
ACCESSION				

VERSION AX196260.1 GI:15386462

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS	Wesche, H. and Li, S.
TITLE	Irak-4: compositions and methods of use
JOURNAL	Patent: WO 0151641-A 2 19-JUL-2001; Tularik Inc. (US)

FEATURES	Location/Qualifiers
source	1. .1383
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/mol_type="unassigned DNA"
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cDNA"

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CDS
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 SDTRHFSFELKLVNNNDERIPISGVNGKKEGGFVGVYVYNNTVAKLTAAIM
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 ASERPAQTVTSKRVGTITAMPEALRGITIKSDIISVAGVLEITITGPAVDHKE
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Query Match	99.5%	Score 292.4;	DB 6;	Length 1383;
Best Local Similarity	99.7%	Pred. No. 4.3e-64;		
Matches 293; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

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25 ACATATGTCGCGTCCCTCAATGTTGACATAATTAGGAAGCTGCAGATTTTATGATCCT 64

[illegible]

121 AATCAGTTTCATTAAGAGATTGAAACATTACTTCAAACTGAAAAAGTCCCACTTCT 180

QY 181 GAATTACTGTTGACTGGGGACCAAAATTGCACAGTTGTGATCTTGTGATCTTTTG 240

241 ATCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCCC 294

	RESULT_13	
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LOCUS	Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4)	1383 bp mRNA linear PRI 20-APR-2002
DEFINITION		
ACCESSION	AF445802	mRNA, complete cds.
VERSION	AF445802.1	GI:20219009
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Li, S., Strelow, A., Fontana, E.J. and Wesche, H.	
TITLE	IRAK-4: a novel member of the IRAK family with the properties of an IRAK-kinase	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)	
MEDLINE	21957277	
PUBMED	11960013	
REFERENCE	2 (bases 1 to 1383)	
AUTHORS	Suzuki, N., Suzuki, S., Duncan, G.S., Miller, D.G., Wada, T., Mesches, C., Takada, H., Wakeham, A., Itie, A., Li, S., Penninger, J.M., Weesche, H., Ohashi, P.S., Mak, T.W. and Yeh, W.C.	
TITLE	Severe impairment of interleukin-1 and Toll-like receptor signalling in mice lacking IRAK-4	
JOURNAL	Nature 416 (6882), 750-756 (2002)	
MEDLINE	21959395	
PUBMED	11923871	
REFERENCE	3 (bases 1 to 1383)	
AUTHORS	Li, S., Strelow, A., Fontana, E.J. and Wesche, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-NOV-2001) Biology I, Tulatix Inc., 2 Corporate Drive, South San Francisco, CA 94080, USA	
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Query Match	99.5%; Score 292.4; DB 9; Length 1383;	
Best Local Similarity	99.7%; Pred. No. 4.3e-64;	
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D7	61 CAAGAAGATGGAAGAACTTAGCTTGACTTAATAAAAACAATCTGGTGAATGATGATAC 120	
D8	85 CAAGAAGATGGAAGAAAGTGTGCTGCTATTAATAAAAAACAATCTGGTGAATGATGATAC 144	

OY		121	AATGAGTTTCACTAAGAAGATTGGTAGCATTAACCTTGAAAAGTCACCATTCT	180
Db		145	AATCAGTTTTACAATAAGAGATTTGAAGCATTAATTCAAACGTGAAAAAGCCACTTCT	204
OY		181	GAA TTACT GT T G TG A C T G G G G C A C C A C A A A T T G C A C A G T T G G T G A T C T T T G T G A T C T T T T Y G	240
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OY		241	A TC CA AA AT GA MA T T T T T T G C T C C T G C G A G T C T T T T G C T C C A G A T G C T G T T C C	294
Db		265	A TC CA AA AT GA MA T T T T T T T T T T T T T G C T C C T G C A G T C T T T T G C T C C A G A T G C T G T T C C	318
RESULT_14				
LOCUS			AYZ83670	1383 bp mRNA linear PRI 17-JUN-2003
DEFINITION			Homo sapiens interleukin-1 receptor associated kinase 4 mutant form	
ACCESSION			AYZ83670	
VERSION			AYZ83670.1	GI:31871817
KEYWORDS			.	
SOURCE			Homo sapiens	(human)
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS			Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G.,	
TITLE			Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient With Recurrent Bacterial Infections	
JOURNAL REFERENCE			J. Exp. Med. (2003) In press	
AUTHORS			Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.	
TITLE			Direct Submission Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA	
FEATURES			location/Qualifiers	
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			/isolation_source="patient hyporesponsive to lipopolysaccharide and interleukin-1 and suffering from recurrent bacterial infections"	
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			877	/gene="IRAK4"
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			/replace="c"	

ORIGIN

Query Match 99.5%; Score 292.4; DB 9; Length 1383;
 Best Local Similarity 99.7%; Pred. No. 4.3e-64;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGTCGGCTGCTCAATGTTGACCTAATTAAGAGCTGTCAGATTTTATGATCCT 60
 DB 25 ACATATGTCGGCTGCTCAATGTTGACCTAATTAAGAGCTGTCAGATTTTATGATCCT 84

QY 61 CAAGAAGATGGAAGAAGTTAGCTGATTAATAAAACCATCTGTCATGATAGTAC 120
 DB 85 CAAGAAGATGGAAGAAGTTAGCTGATTAATAAAACCATCTGTCATGATAGTAC 144

QY 121 AATCAGTTTCACATTAAGAGATTGAAGCATTAATTAAGTGAAGTGAAGTCCACTTCT 180
 DB 145 AATCAGTTTCACATTAAGAGATTGAAGCATTAATTAAGTGAAGTGAAGTCCACTTCT 204

QY 181 GAATTAAGTCTGTTGACTGGGGACACCAAAATGACAGCTGTCATCTTTGATCTTTTG 240
 DB 205 GAATTAAGTCTGTTGACTGGGGACACCAAAATGACAGCTGTCATCTTTGATCTTTTG 264

QY 241 ATCCAAATGAATTTTGTCTCTGAGATCTTTGTCTCCAGATGCTGTCC 294
 DB 265 ATCCAAATGAATTTTGTCTCTGAGATCTTTGTCTCCAGATGCTGTCC 318

RESULT 15
 BC013316 1629 bp mRNA linear PRI 30-JUN-2004
 LOCUS Homo sapiens interleukin-1 receptor-associated kinase 4, mRNA (CDNA
 DEFINITION Clone MGC:13350 IMAGE:4287014), complete cds.
 ACCESSION BC013316
 VERSION BC013316.1 GI:15426431
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1629)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klusner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schlier, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, U., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Lott, J., Lott, J., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McKernan, P.D., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Valle, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shvachenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, D.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M., Butler, J., Schein, J.E., Jones, S.J., and Marra, M.A.
 Butcherfield, J., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL JOURNAL
 PUBLISHED 12/7/99
 REFERENCE 2 (bases 1 to 1629)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadn@systemsbio.org
 Anup Madan, Jeesita Fahy, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
 Series: IRAL Plate: 19 Row: n Column: 24
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="MGC:13350 IMAGE:4287014"
 /issue_type="Brain, Primitive neuroectodermal"
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 /lab_host="DH10B"
 /note="Vector: pDNR-LIB"
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 /note="synonyms: NY-REN-64, REN64"
 /db_xref="LOCUSID:51135"
 /db_xref="MIM:606883"
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 /db_xref="LOCUSID:51135"
 /db_xref="MIM:606883"
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 LDGPRPSIMHMKCKIAOGANGINLHNHHDIDISKANILDEAPAKISDGLAR
 ASERPAQVYMSRIYGTANMAPELAREITPKSDIISFGVILEITIGLPAVDENR
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 QQLQLEMTAS"

ORIGIN

Query Match 99.5%; Score 292.4; DB 9; Length 1629;
 Best Local Similarity 99.7%; Pred. No. 4.3e-64;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGTCGGCTGCTCAATGTTGACCTAATTAAGAGCTGTCAGATTTTATGATCCT 60
 DB 95 ACATATGTCGGCTGCTCAATGTTGACCTAATTAAGAGCTGTCAGATTTTATGATCCT 154

QY 61 CAAGAAGATGGAAGAAGTTAGCTGATTAATAAAACCATCTGTCATGATAGTAC 120
 DB 155 CAAGAAGATGGAAGAAGTTAGCTGATTAATAAAACCATCTGTCATGATAGTAC 214

QY 121 AATCAGTTTCACATTAAGAGATTGAAGCATTAATTAAGTGAAGTGAAGTCCACTTCT 180
 DB 215 AATCAGTTTCACATTAAGAGATTGAAGCATTAATTAAGTGAAGTGAAGTCCACTTCT 274

QY 181 GAATTAAGTCTGTTGACTGGGGACACCAAAATGACAGCTGTCATCTTTGATCTTTTG 240
 DB 275 GAATTAAGTCTGTTGACTGGGGACACCAAAATGACAGCTGTCATCTTTGATCTTTTG 334

QY 241 ATCCAAATGAATTTTGTCTCTGAGATCTTTGTCTCCAGATGCTGTCC 294
 DB 335 ATCCAAATGAATTTTGTCTCTGAGATCTTTGTCTCCAGATGCTGTCC 388

Search completed: January 12, 2005, 05:06:47

Job time : 1848 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 10, 2005, 23:07:39 ; Search time 152 seconds
(without alignments)
231.286 Million cell updates/sec

Title: US-10-001-254-6
Perfect score: 517
Sequence: 1 TYVRCLNVGLIRKLSDFIDP.....LLIQNEFPAPALLPDAVP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	98	5	AAE24854 Human IRA
2	517	100.0	98	5	AAE38897 Human IRA
3	517	100.0	206	3	AAV92347 Human can
4	517	100.0	455	4	ABG12618 Novel hum
5	517	100.0	460	5	AAE24859 Human IRA
6	517	100.0	460	5	AAE24865 Human IRA
7	517	100.0	460	5	AAE38908 Human IRA
8	517	100.0	460	5	AAE38902 Human IRA
9	517	100.0	460	6	ABR44401 Human IL-
10	517	100.0	460	8	ADO44001 Amino aci
11	513	99.2	191	4	AAE05402 Truncated
12	513	99.2	460	4	AAE05398 Human int
13	513	99.2	460	4	AAE05401 Human IRA
14	511	98.8	460	4	AAE05403 Human IRA
15	507	98.1	460	4	AAE05404 Human IRA
16	476	92.1	459	4	AAE05399 Mouse int
17	473	91.5	459	4	AAE05405 Mouse IRA
18	473	91.5	459	4	AAE05406 Mouse IRA
19	256	49.5	102	4	ABG12616 Novel hum
20	247	47.8	59	5	AAE24864 Human IRA
21	247	47.8	59	5	AAE38907 Human IRA
22	247	47.8	60	8	ABE28317 Human KRP
23	245	47.4	127	4	ABG12615 Novel hum
24	96.5	18.7	596	3	AAV69406 A human i
25	96.5	18.7	596	4	AAE65667 Novel p

26	96.5	18.7	596	4	AAE48173 Interleuk
27	96.5	18.7	596	8	AD129275 Human MAR
28	96.5	18.7	597	4	AAE48172 Interleuk
29	96.5	18.7	599	4	AAE38644 Human pol
30	96.5	18.7	622	4	ABG22715 Novel hum
31	95	18.4	609	7	ADB61346 Murine IR
32	84	16.2	497	2	ABG03007 Novel hum
33	79	15.3	590	2	AAV08653 Human IRA
34	79	15.3	590	7	ADE04441 Human IRA
35	79	15.3	625	2	AAV08654 Human IRA
36	77	14.9	251	6	AAE37948 Murine My
37	72.5	14.0	813	5	AAU97836 Human cys
38	72.5	14.0	824	3	AAE41026 Human ORF
39	72.5	14.0	824	5	ABP61489 Human NF-
40	72.5	14.0	824	5	AAU97838 Human cys
41	72.5	14.0	824	8	ADN04325 Antispori
42	72.5	14.0	824	8	ADP82021 Human muc
43	72	13.9	462	4	ABE65115 Drosophi
44	71.5	13.8	5836	8	ADK16042 Streptomy
45	71	13.7	259	7	ADF30722 Rat angio

ALIGNMENTS

RESULT 1	AAE24854
ID	AAE24854 standard; peptide: 98 AA.
XX	AAE24854:
AC	
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Human IRAK4 DD (death domain) protein.
XX	
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy.
KW	Homo sapiens.
OS	
XX	
PN	WO200240680-A2.
XX	
PD	23-MAY-2002.
XX	
PF	15-NOV-2001; 2001WO-US044844.
XX	
PR	17-NOV-2000; 2000US-00715893.
PR	29-JUN-2001; 2001US-0301889P.
PA	(BURN-) BURHAM INST.
XX	
PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W; Stenmer-Liwen F;
PI	WPI; 2002-500222/53.
DR	N-PSDB; AAD40074.
XX	
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
PT	Claim 1; Page 174; 209pp; English.
PS	
XX	
CC	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDB (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent,

by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD protein

Query Match 100.0%; Score 517; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLANGLIRKLSDFIDPEGWKLAIVAIKPSGDRNQHIFRFEALLQTKSPS 60
DB 1 TYRCLANGLIRKLSDFIDPEGWKLAIVAIKPSGDRNQHIFRFEALLQTKSPS 60
QY 61 ELFPDMGTNCTGVGDVLDLILQNEFFAPASLLPDVAVP 98
DB 61 ELFPDMGTNCTGVGDVLDLILQNEFFAPASLLPDVAVP 98

RESULT 2
AAE38897 standard; protein; 98 AA.
AAE38897;

18-DEC-2003 (first entry)

Human IRAK4 DD protein.

Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neutral growth factor receptor-interacting protein; cell adhesion; vasculitis; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hyperplasia; antibacterial; NIDP; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK.

Homo sapiens.

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

PA (REED/) REED J C.
PA (GODZIK/) GODZIK A.
PA (PAWLOWSKI/) PAWLOWSKI K.
PA (FLORENTINO L.) FLORENTINO L.
PA (LEES S H.) LEES S H.
PA (ROTH W.) ROTH W.
PA (STENNER-LIEMEN F.) STENNER-LIEMEN F.

XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Steiner-Liemen F;
XX WPI; 2002-500222/53.
DR N-PSDB; AAD59056.
XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 1; Page 34; 99pp; English.

The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neutral growth factor receptor-interacting protein (NIDP) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDP with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DEDs and NB-ARC domains and/or anti-DD or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, hyperplasia, neoplasia, keloid, benign prostatic hyperplasia, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 DD protein

Query Match 100.0%; Score 517; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLANGLIRKLSDFIDPEGWKLAIVAIKPSGDRNQHIFRFEALLQTKSPS 60
DB 1 TYRCLANGLIRKLSDFIDPEGWKLAIVAIKPSGDRNQHIFRFEALLQTKSPS 60
QY 61 ELFPDMGTNCTGVGDVLDLILQNEFFAPASLLPDVAVP 98
DB 61 ELFPDMGTNCTGVGDVLDLILQNEFFAPASLLPDVAVP 98

RESULT 3
AA92347 standard; protein; 206 AA.
AA92347;

10-AUG-2000 (first entry)

Human cancer associated antigen precursor from clone NY-BEN-64.

renal cancer; cancer associated antigen precursor; diagnosis; cytostatic.

Homo sapiens.

WO200020587-A2.

13-APR-2000.

04-OCT-1999; 99WO-US022873.

05-OCT-1998; 98US-00166300.

PR 05-OCT-1998; 98US-00166350.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 PI Obata Y, Gout I, Tureci O, Sahin U, Pfeundschnuh M, Scanlan MJ;
 PI Stockert B, Chen Y, Old LJ, Jager B, Knuth A;
 XX WPI: 2000-303774/26.
 DR N-PSDB; AAA09319.
 XX
 PT Preventing, diagnosing and/or treating disorders associated with abnormal
 PT expression of human cancer associated antigens.
 XX
 PS Example 1; Page 92-93; 121pp; English.
 XX
 CC AA92338-47 are encoded by novel genes isolated by SEREX screening from a
 CC renal cancer cell line 1973/10.4. They are cancer associated antigen
 CC precursors. These gene products are useful in methods for preventing,
 CC diagnosing and/or treating disorders, especially cancer, associated with
 CC abnormal expression of human cancer associated antigens. The method
 CC comprises contacting a sample from a subject with an agent that
 CC specifically binds to the nucleic acid molecule or expression product (or
 CC fragment) complexed with a human leukocyte antigen (HLA) molecule and
 CC determining the interaction between the agent and the nucleic acid
 CC molecule or the expression product as a determination of the disorder
 CC
 SO Sequence 206 AA;

Query Match 100.0%; Score 517; DB 3; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.2e-60;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNGLIRKLSDFIDPQGWKLAVALKKPSGDRYNOFHRRFALLQTKSPTS 60
 Db 9 TYVCLNGLIRKLSDFIDPQGWKLAVALKKPSGDRYNOFHRRFALLQTKSPTS 68
 Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASILLPDAPV 98
 Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASILLPDAPV 106

RESULT 4
 ABG12618
 ID ABG12618 standard; protein; 455 AA.
 XX
 AC ABG12618;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #12609.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PP 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS76805.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 42977; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 455 AA;
 Query Match 100.0%; Score 517; DB 4; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.5e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNGLIRKLSDFIDPQGWKLAVALKKPSGDRYNOFHRRFALLQTKSPTS 60
 Db 9 TYVCLNGLIRKLSDFIDPQGWKLAVALKKPSGDRYNOFHRRFALLQTKSPTS 68
 Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASILLPDAPV 98
 Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASILLPDAPV 106

RESULT 5
 AAE24859
 ID AAE24859 standard; protein; 460 AA.
 XX
 AC AAE24859;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Human IRAK4 protein #1.
 XX
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200240680-A2.
 XX
 PD 23-MAY-2002.
 XX
 PP 15-NOV-2001; 2001WO-US044844.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PI Steiner-Liwen F;
 XX WPI; 2002-500222/53.
 DR N-PSDB; AAD40079.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 3; Page 183-184; 209pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC creating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 protein
 XX
 SQ Sequence 460 AA;
 Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINLVGLIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHIRFALLQTGKSPS 60
 DB 9 TYVRCINLVGLIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHIRFALLQTGKSPS 68
 QY 61 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDAVP 98
 DB 69 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDAVP 106
 RESULT 6
 AAE24865
 ID AAE24865 standard; protein; 460 AA.
 AC AAE24865;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Human IRAK4 protein #2.
 XX
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200240680-A2;
 XX

PD 23-MAY-2002.
 XX
 XX 15-NOV-2001; 2001WO-US044844.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (BURN-) BURHAM INST.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Steiner-Liwen F;
 XX
 DR WPI; 2002-500222/53.
 DR N-PSDB; AAD40085.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 1; Page 196-197; 209pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC creating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 protein
 XX
 SQ Sequence 460 AA;
 Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINLVGLIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHIRFALLQTGKSPS 60
 DB 9 TYVRCINLVGLIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHIRFALLQTGKSPS 68
 QY 61 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDAVP 98
 DB 69 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDAVP 106
 RESULT 7
 AAE38908
 ID AAE38908 standard; protein; 460 AA.
 AC AAE38908;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human IRAK4 protein #2.
 XX

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting protein; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDP;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; interleukin-1 receptor-associated kinase; IRAK.
 XX
 OS Homo sapiens.
 XX
 PN US2003049702-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 15-NOV-2001; 2001US-00001254.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 17-NOV-2000; 2000US-0367360P.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (REED/) REED J C.
 PA (GODZ/) GODZIK A.
 PA (PAMU/) PAWLOWSKI K.
 PA (FIOR/) FIORENTINO L.
 PA (LEES/) LEE S H.
 PA (ROTH/) ROTH W.
 PA (STEN/) STENNER-LIEWEN F.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liewen F;
 XX
 PI WPI: 2002-500222/53.
 DR N-PSDB; AAD59067.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 1; Page 53-54; 99pp; English.
 XX
 CC The present invention provides novel death Domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDP). DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDP, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC Interleukin-1 receptor-associated kinase (IRAK)-4 protein
 CC
 XX
 SQ Sequence 460 AA;
 Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-55;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 TYVCLNVGLIRKLSDFIDPOEGWKLAVALIKPSGDRYNQFIIRFEALLQTGKSPTS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 9 TYVCLNVGLIRKLSDFIDPOEGWKLAVALIKPSGDRYNQFIIRFEALLQTGKSPTS 68
 QY 61 ELFPDMGTNTGYDLVDLILQNEFPAPASILLDPDAVP 98
 DB 69 ELFPDMGTNTGYDLVDLILQNEFPAPASILLDPDAVP 106
 RESULT 8
 AAE38902
 ID AAE38902 standard; protein; 460 AA.
 XX
 AC AAE38902;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human IRAK4 protein #1.
 XX
 KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting protein; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDP;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; interleukin-1 receptor-associated kinase; IRAK.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 9..106
 FT /note="Death domain of IRAK-4"
 XX
 XX US2003049702-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 15-NOV-2001; 2001US-00001254.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 17-NOV-2000; 2000US-0367360P.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (REED/) REED J C.
 PA (GODZ/) GODZIK A.
 PA (PAMU/) PAWLOWSKI K.
 PA (FIOR/) FIORENTINO L.
 PA (LEES/) LEE S H.
 PA (ROTH/) ROTH W.
 PA (STEN/) STENNER-LIEWEN F.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liewen F;
 XX
 PI WPI: 2002-500222/53.
 DR N-PSDB; AAD59061.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 2; Fig 10B; 99pp; English.
 XX
 CC The present invention provides novel death Domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDP). DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDP, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC Interleukin-1 receptor-associated kinase (IRAK)-4 protein
 CC
 XX

CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. Dbs, Dps and NB-ARC
 CC domain and/or anti-DB, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 protein
 XX

SO Sequence 460 AA;

Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVGLIRKLSDFIDPQEGWKLAVALIKPSGDDRYNQFHRRFALLQTKSPPTS 60
 DB 9 TYRCLNVGLIRKLSDFIDPQEGWKLAVALIKPSGDDRYNQFHRRFALLQTKSPPTS 68
 61 ELFPDGTCTGVDVLDLIONEFPAPASILLPDAPV 98
 69 ELFPDGTCTGVDVLDLIONEFPAPASILLPDAPV 106

RESULT 9
 ID ABR44401 standard; protein; 460 AA.
 XX ABR44401;

DT 11-UTL-2003 (first entry)
 DE Human IL-1 receptor-associated kinase-4 amino acid sequence.

KM Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KM interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KM inflammatory disease; infection; diagnostic; therapeutic; prophylaxis.
 OS Homo sapiens.

PN WO2003028636-A2.

PD 10-APR-2003.

PF 26-SEP-2002; 2002WO-US030574.

PR 28-SEP-2001; 2001US-00966451.

PA (ISIS-) ISIS PHARM INC.

PI Bennett FC, Freiler SM;

DR WPI; 2003-363256/34.

DR N-PSDB; ACC47548.

PT New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX

PS Example 13; Page 80-83; 119pp; English.

CC The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or

CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence
 CC represents the human IL-1 receptor-associated kinase-4 amino acid
 CC sequence
 XX

SO Sequence 460 AA;

Query Match 100.0%; Score 517; DB 6; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVGLIRKLSDFIDPQEGWKLAVALIKPSGDDRYNQFHRRFALLQTKSPPTS 60
 DB 9 TYRCLNVGLIRKLSDFIDPQEGWKLAVALIKPSGDDRYNQFHRRFALLQTKSPPTS 68
 61 ELFPDGTCTGVDVLDLIONEFPAPASILLPDAPV 98
 69 ELFPDGTCTGVDVLDLIONEFPAPASILLPDAPV 106

RESULT 10
 ID ADO44001 standard; protein; 460 AA.
 XX ADO44001;

DT 15-UTL-2004 (first entry)
 DE Amino acid sequence of human IRAK4.

KM protein complex; neurological disease; stroke; neurodegeneration;
 KM Wallerian degeneration; Alzheimer's disease; neurological disorder;
 KM epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
 KM atherosclerosis; 1D-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;
 KM ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;
 KM Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;
 KM FLJ14653 NT2R2002252; FLJ30839 PEBBA2002429; HERC2;
 KM inositol polyphosphate-5-phosphatase; inositol-1; 4;
 KM 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;
 KM Nek3; Pak3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;
 KM Pushover; S-adenosylhomocysteinease;
 KM secretory carrier-associated membrane protein 2; surfactant protein 2;
 KM ubiquitin carboxyl terminal hydrolase 11;
 KM upstream regulatory element binding protein 1; Vartul;
 KM Werner's syndrome helicase interacting protein; WHIP;
 KM X-ray repair cross complementing protein 4.

OS Homo sapiens.

PN WO2004031242-A2.

PD 15-APR-2004.

PF 11-SEP-2003; 2003WO-EP010110.

PR 12-SEP-2002; 2002EP-00020495.

PR 12-SEP-2002; 2002EP-00020496.

PR 12-SEP-2002; 2002EP-00020497.

PA (CELL-) CELLZOME AG.

PI Bouwmeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;

PI Kuester B, Hopf C;

DR WPI; 2004-316467/29.

CC New complex comprising at least one first protein, and at least one
 CC second protein, useful for treating stroke, Alzheimer's disease,
 CC neurological disorders such as epilepsy, and inflammatory conditions such
 CC as ulcerative colitis.
 XX

PS Example, Page 213-214, 287pp; English.

XX The specification describes protein complexes involved in cellular

CC processes which have been shown to be critical for the development of

CC various forms of neurological diseases. Three protein complexes were

CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3

CC protein complex. The protein complex are useful for treating diseases and

CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,

CC Alzheimer's disease, neurological disorders such as epilepsy, and

CC inflammatory conditions such as ulcerative colitis, Crohn's disease or

CC atherosclerosis. Proteins identified as being part of the protein

CC complexes of the invention are ID-MYO-Inositol triphosphate 3 kinase A,

CC ASK1, ASK2, ASK3, CamKII Beta, CamKII gamma, casein kinase

CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,

CC FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical

CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,

CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1411,

CC MstP030, Nek3, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1

CC precursor, Pushover, a putative S-adenosylhomocysteine, secretory

CC carrier-associated membrane protein 2, surfactant locus protein 2, ubiquitin

CC carboxyl terminal hydrolase 11, upstream regulatory element binding

CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),

CC X-ray repair cross complementing protein 4 (isoform 1). The present

CC sequence represents IRAK4.

XX

SQ Sequence 460 AA;

Query Match 100.0%; Score 517; DB 8; Length 460;

Best Local Similarity 100.0%; Pred. No. 1.6e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRLKSDFLDPBGWKKLAVALIKKPSGDRYNOFIRREALLQTKSPTS 60

Db 9 TYVCLNVLGRLKSDFLDPBGWKKLAVALIKKPSGDRYNOFIRREALLQTKSPTS 68

Qy 61 ELFPDWTGTTCTAGDVLVDLLIQNEFPAPASLLPDAVP 98

Db 69 ELFPDWTGTTCTAGDVLVDLLIQNEFPAPASLLPDAVP 106

RESULT 11

AAE05402 standard; protein, 191 AA.

XX

AC AAE05402;

DT 24-SEP-2001 (first entry)

XX

DE Truncated form of human IRAK-4 protein.

XX

Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;

KM IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;

KM chronic obstructive pulmonary disease; neuroprotective; chronic cough;

KM adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;

KM interstitial lung disease; allergic rhinitis; transplant rejection;

KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;

KM multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;

KM cardiovascular disease; atherosclerosis; neurodegenerative disease;

KM sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;

KM inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;

KM Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;

KM sarcoidosis; transgenic animal; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN MO200151641-A1.

XX

PD 19-JUN-2001.

XX

PF 12-JAN-2001; 2001WO-US001171.

XX

PR 13-JAN-2000; 2000US-0176395P.

XX (TULIA-) TULARIX INC.

PA

XX

PI Mesche H, Ld S;

XX

DR WPI; 2001-451860/48.

XX

PT Novel human interleukin-1 receptor associated kinase polypeptide, useful

PT for identifying modulators of the polypeptide for treating gout, asthma,

PT allergic rhinitis, multiple sclerosis and skin cancer.

XX

ES Claim 53; Page: 89pp; English.

XX

CC The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)

CC -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18

CC and other receptors and act to transduce signals originating from the

CC activated receptors, ultimately leading to a variety of downstream

CC effects such as nuclear factor (NF)-kappa activation. The IRAK-4

CC inhibitors are useful for treating inflammatory diseases such as

CC pulmonary diseases and diseases of the airway (e.g., adult respiratory

CC disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),

CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or

CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,

CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or

CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),

CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of

CC the central nervous system (e.g., neurodegenerative disease), CD14

CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,

CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic

CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and

CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,

CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of

CC IRAK-4 activity or expression are used to inhibit signal transduction

CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll

CC receptor in a cell. They also inhibit the activation of a transcription

CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a

CC nonhuman transgenic animal which is useful for testing the function of

CC IRAK-4 in vivo, to generate models for the study of inflammatory

CC disorders and conditions and for the development of potential treatments

CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences

CC are also used in gene therapy and in antisense therapy. The present

CC sequence is the truncated form of human IRAK-4 protein. This sequence was

CC constructed by deleting the residues after K191 in the wild type human

CC IRAK-4 protein. This truncated form is the dominant negative form of

CC human IRAK-4 protein. Note: This sequence is not shown in the

CC specification but is derived from human IRAK-4 (SEQ ID NO: 1) shown in

CC figure 1 of the specification (AAE05398)

XX

SQ Sequence 191 AA;

Query Match 99.2%; Score 513; DB 4; Length 191;

Best Local Similarity 99.0%; Pred. No. 1.6e-55;

Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRLKSDFLDPBGWKKLAVALIKKPSGDRYNOFIRREALLQTKSPTS 60

Db 9 TYVCLNVLGRLKSDFLDPBGWKKLAVALIKKPSGDRYNOFIRREALLQTKSPTS 68

Qy 61 ELFPDWTGTTCTAGDVLVDLLIQNEFPAPASLLPDAVP 98

Db 69 ELFPDWTGTTCTAGDVLVDLLIQNEFPAPASLLPDAVP 106

RESULT 12

AAE05398 standard; protein, 460 AA.

XX

AC AAE05398;

DT 24-SEP-2001 (first entry)

XX

DE Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 protein.

XX

Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal.

Homo sapiens.

Key Location/Qualifiers
 5..147
 Domain /label= Death_domain
 /note= "Also known as N-terminal domain"
 192..460
 Domain /label= Central_kinase_domain

MO200151641-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001171.

13-JAN-2000; 2000US-0176395P.

(TUL-) TULARIK INC.

Wesche H, Li S;
 WPI; 2001-451860/48.
 N-PSDB; AAD10197.

Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

Claim 17; Fig 1; 89pp; English.

The present sequence is human interleukin (IL)-1 receptor associated kinase (IRAK)-4 protein. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, sarcoidosis and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NFkappaB in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy.

Sequence 460 AA;

Query Match 99.2%; Score 513; DB 4; Length 460;
 Best Local Similarity 99.0%; Pred. No. 5.3e-59;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TYRCLAVGILRLSPFIDPOGKMLAVAKKPSGDRYNOFHRREALLOGKSPTS 60
 9 TYRCLAVGILRLSPFIDPOGKMLAVAKKPSGDRYNOFHRREALLOGKSPTS 68

61 ELFPDWTNCTVGDVLDLLIQNEFPAPASLLPDAVP 98
 69 ELFPDWTNCTVGDVLDLLIQNEFPAPASLLPDAVP 106

RESULT 13
 AAE05401
 ID AAE05401 standard; protein; 460 AA.
 XX
 AC AAE05401,
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human IRAK-4 mutant (K213A, K214A).
 XX
 KW Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; mutant; mutein.
 KW
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 213 /note= "Wild type Lys substituted with Ala"
 FT Misc-difference 214 /note= "Wild type Lys substituted with Ala"
 FT
 PN MO200151641-A1.
 XX
 PD 19-JUL-2001.
 PF 12-JAN-2001; 2001WO-US001171.
 PR 13-JAN-2000; 2000US-0176395P.
 PA (TUL-) TULARIK INC.
 PI Wesche H, Li S;
 WPI; 2001-451860/48.

Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

Claim 51; Page; 89pp; English.

The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)-4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory

CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
CC the central nervous system (e.g., neurodegenerative disease), CD14
CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
CC dermatitis, inflammatory bowel disease (e.g., Crohn's disease and
CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
CC IRAK-4 activity or expression are used to inhibit signal transduction
CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
CC receptor in a cell. They also inhibit the activation of a transcription
CC factor that activates NF-kappaB in the cell. IRAK-4 is used to create a
CC nonhuman transgenic animal which is useful for testing the function of
CC IRAK-4 in vivo, to generate models for the study of inflammatory
CC disorders and conditions and for the development of potential treatments
CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
CC are also used in gene therapy and in antisense therapy. The present
CC sequence is a mutant (K213A, K214A) of human IRAK-4 protein. Note: This
CC sequence is not shown in the specification but is derived from human IRAK
CC -4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398)
XX
SQ Sequence 460 AA;

Query Match 99.2%; Score 513; DB 4; Length 460;
Best Local Similarity 99.0%; Pred. No. 5.3e-59;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPEGWKLAVAIKKSPGDRYQFIRFEALLQTKSPSTS 60
DB 9 TYVCLNGLIRKISDFIDPEGWKLAVAIKKSPGDRYQFIRFEALLQTKSPSTS 68
61 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLPDVAVP 98
DB 69 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLPDVAVP 106

RESULT 14
AAE05403
ID AAE05403 standard; protein; 460 AA.
XX
AC AAE05403;

XX 24-SEP-2001 (first entry)
XX

DE Human IRAK-4 polymorphic variant (I531L).
XX

XX Human: interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
XX IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
XX chronic obstructive pulmonary disease; neuroprotective; chronic cough;
XX adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
XX interstitial lung disease; allergic rhinitis; transplant rejection;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
XX cardiovascular disease; atherosclerosis; neurodegenerative disease;
XX sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
XX inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
XX Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
XX sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism.
XX

OS Homo sapiens.
OS Synthetic.
XX

XX Key Location/Qualifiers
XX

XX Misc-difference 53 /note= "Wild type Ile substituted with Leu"
XX

XX WO200151641-A1.
XX

XX 19-JUL-2001.
XX
PD

XX 12-JAN-2001; 2001WO-US001171.
XX
XX 13-JAN-2000; 2000US-0176395P.
XX
XX (TTLA-) TTLARIK INC.
XX
XX Wesche H, Li S;
XX
XX WPI; 2001-451860/48.
XX

XX Novel human interleukin-1 receptor associated kinase polypeptide, useful
XX for identifying modulators of the polypeptide for treating gout, asthma,
XX allergic rhinitis, multiple sclerosis and skin cancer.
XX

XX Disclosure; Page: 89pp; English.
XX

XX The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)
XX -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18
XX and other receptors and act to transduce signals originating from the
XX activated receptors, ultimately leading to a variety of downstream
XX effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
XX inhibitors are useful for treating inflammatory diseases such as
XX pulmonary diseases and diseases of the airway (e.g., adult respiratory
XX disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
XX pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
XX allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
XX diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
XX cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
XX the central nervous system (e.g., neurodegenerative disease), CD14
XX mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
XX psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
XX dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
XX ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
XX sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
XX IRAK-4 activity or expression are used to inhibit signal transduction
XX resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
XX receptor in a cell. They also inhibit the activation of a transcription
XX factor that activates NF-kappaB in the cell. IRAK-4 is used to create a
XX nonhuman transgenic animal which is useful for testing the function of
XX IRAK-4 in vivo, to generate models for the study of inflammatory
XX disorders and conditions and for the development of potential treatments
XX for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
XX are also used in gene therapy and in antisense therapy. The present
XX sequence is a polymorphic variant (I531L) of human IRAK-4 protein. Note:
XX This sequence is not shown in the specification but is derived from human
XX IRAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398)
XX

SQ Sequence 460 AA;

Query Match 99.8%; Score 511; DB 4; Length 460;
Best Local Similarity 99.0%; Pred. No. 9.9e-59;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPEGWKLAVAIKKSPGDRYQFIRFEALLQTKSPSTS 60
DB 9 TYVCLNGLIRKISDFIDPEGWKLAVAIKKSPGDRYQFIRFEALLQTKSPSTS 68
61 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLPDVAVP 98
DB 69 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLPDVAVP 106

RESULT 15
AAE05404
ID AAE05404 standard; protein; 460 AA.
XX
AC AAE05404;

XX 24-SEP-2001 (first entry)
XX

XX Human IRAK-4 polymorphic variant (G17A).
XX
XX

XX Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic;
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasotonic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 17 /note= "Wild type Gly substituted with Ala"
 PT
 PN WO200151641-A1.
 PD 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001171.
 PF
 XX 13-JAN-2000; 2000US-0176395P.
 PR
 XX (TULSA-) TULARIK INC.
 PA
 XX Wesche H, Li S;
 PI
 XX MPI; 2001-451860/48.
 DR
 XX Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Disclosure; Page; 89pp; English.
 XX
 CC The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)
 CC -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18
 CC and other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappa activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis), systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy. The present
 CC sequence is a polymorphic variant (G17A) of human IRAK-4 protein. Note:
 CC This sequence is not shown in the specification but is derived from human
 CC IRAK-4 (SEQ ID NO: 1) shown in Figure 1 of the specification (AAE05398)
 XX

SO Sequence 460 AA;

Query Match 98.1%; Score 507; DB 4; Length 460;
 Best Local Similarity 98.0%; Pred. No. 3.4e-58;
 Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TYRCLAVGLIRKLSPIFDPQSGKKLAVAIKKPSGDDRYNQFHIRREALLQTKSPPTS 60
 DB 9 TYRCLAVGLIRKLSPIFDPQSGKKLAVAIKKPSGDDRYNQFHIRREALLQTKSPPTS 68
 QY 61 ELTFDWTGTTNCTGVDPVLDLLIONEPFAPASLLPDAVP 98
 DB 69 ELTFDWTGTTNCTGVDPVLDLLIONEPFAPASLLPDAVP 106

Search completed: January 10, 2005, 23:21:49
 Job time : 155 secs

R;letsou, A.; Alexander, S.; Orth, K.; Wasserman, S.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 810-814, 1991
A>Title: Generic and molecular characterization of tube, a *Drosophila* gene maternally repressed in the embryo
A.Reference number: A37862; MUID:91126085; PMID:1899484
A.Accession: A37862
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-462 <LETS>
A.Cross-references: UNIPROT:P22812; GB:M59501; NID:g158750; PID:g158751
C.Genetics:
A.Gene: FlyBase:tnb
A.Cross-references: FlyBase:FBgn0003882
C.Superfamily: Drosophila tube protein

Query Match	13.9%	Score 72;	DB 2;	Length 462;
Best Local Similarity	24.8%	Freq. No. 4;		
Matches	28;	Conservative 16;	Mismatches 39;	Indels 30;
			Gaps	
Qy	11	IRKLSDFDPQEGWKLAIVAKRPSGD-----	-RY--	NOHHR 47
		: : : : : : : : :		
Db	41	IYRLAKIIDENSCKRKLMSIT--PKGMDVOACGAGCLNPPAIRKKGFKYTMQDVQIDE		98
		: : : : : : : : :		
Qy	48	FEALLQGSFPTSELFPDWGTT-----	NCTGVDIVDLIIONEEFAPASILLPD	95
		: : : : : : : : :		
Db	99	AANLPPDQGSQWMIIDENKTSGLNRPVYGLIQLLVAAELFSAADFAALD		151

RESULT 3
A24700
apolipoprotein A-I precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: A24700; S00298; A05314
R/Haddad, I.A.; Ocdoyas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A/Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-II, and A-III.
A/Reference: A92558; MUID:87008540; PMID:3020028
A/Accession: A24700

A:Molecule type: DNA
A:Residues: 1-259 <HAD>
A:Cross-references: UNIPROT:P04639; EMBL:J02597; NID:G202935; PIDN:AAA0745.1; PID:G202945
R:Ponch, J.E.; Martial, J.A.; Gilem, J.E.
Eur. J. Biochem. 140, 493-498, 1984
A:Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
A:Reference number: 500298; MUID:84207987; PMID:6426956
A:Accession: 500298
A:Molecule type: mRNA
A:Residues: 1259 <PON>
A:Cross-references: GB:M00001; EMBL:X00558; NID:G202944; PIDN:AAA0749.1; PID:G202945
R:Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Straus, A.W.
J. Biol. Chem. 257, 971-978, 1982
A:Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
A:Reference number: A05314; MUID:82098162; PMID:6798036
A:Accession: A05314

A:Molecule type: protein
A:Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
C:Comment: This protein is synthesized in the liver and small intestine. The propeptide
C:Comment: This protein is a major component of the high density lipoproteins in plasma
C:Genetics:
A:introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 13.7%; Score 71; DB 2; Length 259;
 Best Local Similarity 31.2%; Pred. No. 2.5;
 Matches 24; Conservative 8; Mismatches 31; Indels 14; Gaps 3;

19 DPQEGMKLA-----VAIKPESGDDRYNQFHIRFEALLQTGKSPTESELLFDWGTNCT 72
 ::|::| ||| :
 26 EPQSOMDRYKDFATVYVDADVDSGRDVSQFESSLT-----GQLNLNLIDNWITLGST 79

QY 73 VGDVLDLL-IQNEFFA 87
|||:|:|:|
Db 80 VGRLEQLGPVTQEFWA 96

RESULT 4

type I restriction enzyme M protein - *Helicobacter pylori* (strain 2695)
 C|Species: *Helicobacter pylori*
 C|Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C|Accession: B64626
 R|Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; McNamee,
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
 Nature 388, 539-547, 1997
 A|Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A|Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A|Reference number: A64520; MUID:97394467; PMID:9252185
 A|Accession: B64626
 A|Status: preliminary; nucleic acid sequence not shown; translation not shown
 A|Molecule type: DNA
 A|Residues: 1-527 <TOM>
 A|Cross-references: UNIPROT:Q25521; GB:AE000596; GB:AE000511; NID:92393982; PIDN:AAD0789-
 C|Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match	13.1%	Score 67.5;	DB 2;	Length 527;
Best Local Similarity	31.1%	Pred. No. 15;		
Matches 19;	Conservative 11;	Mismatches 28;	Indels 3;	Gaps 1;

Dy 37 DDKRYNGEHRREFAALL---QTGKSTSELLFDWGTINCTVGLDVLILLIQNEFPAPASILL 93
| : : | : | : : : : : : : : : : : : : : : :
Db 279 DIYSKFHLAGDTLLDPKHEDDEPDAIVSNPYSTKWVDSPILINDERFSPAGYLA 338

QY	94 P 94
Db	339 P 339

RESULT 5
AI0284

```

P:Species exported protein FP02336 (imported) - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #next_change 03-Jul-2004
C:Accession: A10284
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarragge, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Kutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001, MUID:21470413, PMID:11585630
A:Accession: A10284
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:Cross-references: UNIPROT:Q8Z8F8, GB:AL590842, PIDD:G15980333, GSPDB:G1
C:Genetics:
i:Gene: YP02336

```

Query Match	13.0%;	Score 67;	DB 2;	Length 334;
Best Local Similarity	26.5%;	Pred. No. 9,8;		
Matches	22;	Conservative	11;	Mismatches 24;
				Indels 26;
				Gaps 3;

16 DELIDPQEGKKLAVAIKPPSGDGRYNQCHIRREALLOTGKSPTSSELLFDWGTTCNCTGD 75
||| : ||| : : ||| : |||
209 DFLTMDEQWKIGIDGQHSTENSFESFLMR--EKITVDDKSNMS-----TTN----- 254

76 LVNDLLIQNEFFAPASLLLPDAVP 98
 : : |||
 255 -----PMNYITADAPP 265

RESULTS

RESULTS

translation elongation factor EF-Ts - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: G64714
 R:Tomb, J.R.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpi, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: G64714
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-355 <TOM>
 A:Cross-references: UNIPROT:P55975; GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AA00855
 C:Superfamily: translation elongation factor EF-Ts

Query Match 13.0%; Score 67; DB 2; Length 355;
 Best Local Similarity 22.9%; Pred. No. 11;
 Matches 24; Conservative 17; Mismatches 34; Indels 30; Gaps 3;
 Oy 11 IRKLSDFIDPQBGWKKLAVALKPSGDDRYNOFH-----RRFEALLQGTG----- 55
 Db 78 INSEDFVAKNGEKFEL--VKTLTETKANHHTTEELKSPLDNKEFEETLHSGIAVI 134
 Oy 56 -----KSPTELLPDMGTTCVGDVLDLILQNEFFAP 88
 Db 135 GENILVKRIALHAKAPSSHIINGYAHSNARVGLIGIKTDNEKMAP 179

RESULT 7
 576848
 hypothetical protein - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S76848
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76848
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <KAN>
 A:Cross-references: UNIPROT:P74644; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BA1876
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 12.9%; Score 66.5; DB 2; Length 299;
 Best Local Similarity 28.4%; Pred. No. 9.8;
 Matches 23; Conservative 16; Mismatches 37; Indels 5; Gaps 3;
 Oy 12 RKLSDPFDPOBGWKKLAVALKPSGDDRYNOFHRRFEALLQGTGKSPTELLPDMGTN 70
 Db 159 RRLADKLKERLGY--LGYVYKRKPS--HFYRNFSQEKQYEDLSQYREIILISYFDE 214
 Oy 71 CTGVDVLDLILQNEFFAPASL 91
 Db 215 GTVNDLDDQFVNQAFADLAI 235

RESULT 8
 B96633
 hypothetical protein F8A5.28 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96633
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aasen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: B96633
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-491 <STO>
 A:Cross-references: UNIPROT:O22714; GB:AE005173; NID:g2462744; PIDN:AA871963.1; GSPDB:GN
 C:Genetics:
 A:Gene: F8A5.28
 A:Map position: 1

Query Match 12.9%; Score 66.5; DB 2; Length 491;
 Best Local Similarity 26.3%; Pred. No. 18;
 Matches 20; Conservative 15; Mismatches 34; Indels 7; Gaps 2;
 Oy 8 VGLRKLSDFIDPQBGWKKLAVALKPSGDDRYNOFHRRFEALLQGTGKSPTELLPDMG 67
 Db 271 ITLVGRGLKLETVYRIRMSRLAIPTKS-----NVAYLIMIQVLVKLNDLPGAEITLFEW 325
 Oy 68 TTNCCTGD--LVYDLI 81
 Db 326 QANCSYDRIYINVAI 341

RESULT 9
 T50228
 conserved hypothetical protein SPAC607.08c [imported] - fission yeast (Schizosaccharomyces
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T50228
 R:Zimmermann, W.; Wandt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1999
 A:Reference number: Z25047
 A:Accession: T50228
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-579 <ZIM>
 A:Cross-references: UNIPROT:Q9US10; EMBL:AL135751; PIDN:CAB63795.1; GSPDB:GN00066; SPDB:
 A:Experimental source: strain 972h(-); cosmid c607
 C:Genetics:
 A:Gene: SPDB:SPAC607.08c
 A:Map position: 1
 C:Superfamily: Caenorhabditis elegans hypothetical protein F35D1.3

Query Match 12.9%; Score 66.5; DB 2; Length 579;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 28; Conservative 13; Mismatches 39; Indels 11; Gaps 5;
 Oy 6 LNVGLRKLSDFIDPQBGWKKLAVALKPSGDDRYN-QFHRRFEALLQGTGKSPTELLF 64
 Db 268 VTIGISGMLGDYNEVDAMKSLTVGDKSYWGDYALKFEV--EALVDLGRS--LSRLTF 323
 Oy 65 DMGTTCVGDVLDLILQNEFFAP-ASLLLP 94
 Db 324 SAG-----LGMVKGSEVISRTILAPLAAALWP 349

RESULT 10
 T30213
 G-caderlin - sea urchin (Lytechinus variegatus)
 C:Species: Lytechinus variegatus (variegated urchin)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30213
 R:Miller, J.R.; McClay, D.R.
 Dev. Biol. 192, 323-339, 1997

sucrose 1F-fructosyltransferase (EC 2.4.1.99) - wheat
 Alternate names: 1-SST; fructosyltransferase 2; Wf2 protein
 Species: *Triticum aestivum* (common wheat)

C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7906
R;Kiwakami, A.; Yoshida, M.
Bioesi. Biotechnol. Biochem. 66, 2297-2305, 2002
A;Title: Molecular characterization of sucrose:sucrose 1-fructosyltransferase and sucrose
A;Reference number: JC7905; PMID:22394650; PMID:12506944
A;Accession: JC7906
A;Molecule type: mRNA
A;Residues: 1-662 <KAM>
A;Cross-references: UNIPROT:O8W430; DDBJ:AB029888
C;Comment: This enzyme, which is a vacuole-type fructosyltransferase and a fructan-biosyn-
fers a fructosyl moiety from one sucrose to another, resulting in the formation of trises
C;Genetics:
A;Gene: wfc2
C;Keywords: glycosyltransferase; hexosyltransferase

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 10, 2005, 23:08:19 ; Search time 193 Seconds
(without alignments)
292.159 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
Sequence: 1 TTYRCLNVGLIRKLSDFIDP.....LLIQNEFPAPASLLLPDPAVP 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	100.0	460	1 IRA4_HUMAN	Q9NWZ3 homo sapien
2	513	99.2	218	2 Q7Z6A7	Q7Z6A7 homo sapien
3	513	99.2	292	2 Q7Z6A8	Q7Z6A8 homo sapien
4	476	92.1	197	2 Q9D250	Q9D250 mus musculu
5	476	92.1	459	1 IRA4_MOUSE	Q814K2 mus musculu
6	287	55.5	382	2 Q7ZVW7	Q7ZVW7 brachydanto
7	287	55.5	483	2 Q6IWL3	Q6IWL3 brachydanto
8	287	55.5	609	2 AAT37635	AAT37635 brachydanto
9	98.5	19.1	609	2 Q8C7U8	Q8C7U8 mus musculu
10	98.5	19.1	609	2 Q8C840	Q8C840 mus musculu
11	96.5	18.7	596	2 Q9Y616	Q9Y616 homo sapien
12	96.5	18.7	596	2 AAH57800	AAH57800 homo sapi
13	96.5	18.7	596	2 AAH69388	AAH69388 homo sapi
14	95	18.4	609	2 Q8K4B2	Q8K4B2 mus musculu
15	88	17.0	296	2 Q6Y1S1	Q6Y1S1 rattus norv
16	88	17.0	296	2 AAQ91937	AAQ91937 rattus norv
17	86	16.6	672	2 Q7ZYE4	Q7ZYE4 xenopus lae
18	82	15.9	162	1 Q8C1X0	Q8C1X0 mus musculu
19	82	15.9	296	1 MYR8_MOUSE	P23366 mus musculu
20	79	15.3	590	1 IRA2_HUMAN	Q4187 homo sapien
21	75.5	14.6	257	2 Q347Z4	Q347Z4 bacillus su
22	74.5	14.4	550	2 Q9D150	Q9D150 mus musculu
23	74.5	14.4	550	2 Q8VC10	Q8VC10 mus musculu
24	73.5	14.2	539	2 Q6PB60	Q6PB60 mus musculu
25	73.5	14.2	539	2 AAH59871	AAH59871 mus muscu
26	72.5	14.0	824	1 MLT1_HUMAN	Q94D98 homo sapien
27	72	13.9	462	1 TUBE_DROME	P22812 drosophila
28	71.5	13.8	562	1 Q8DM16	Q8DM16 synecococc
29	71.5	13.8	1076	1 HSER_CAVPO	P70106 cavia porce
30	71.5	13.8	5826	2 Q76KY0	Q76KY0 streptomyc
31	71.5	13.8	5826	2 BAD08373	BAD08373 streptomyc

32	71	13.7	259	1 APA1_RAT	P04639 rattus norv
33	71	13.7	1411	2 Q6FSJ5	Q6FSJ5 candida gla
34	70.5	13.6	151	2 Q8CC82	Q8CC82 mus musculu
35	70.5	13.6	565	2 Q8BRV5	Q8BRV5 pseudomonas
36	70.5	13.6	574	2 Q6YB80	Q6YB80 mus musculu
37	70.5	13.6	574	2 Q8C5W0	Q8C5W0 mus musculu
38	70.5	13.6	574	2 AAQ24762	AAQ24762 mus muscu
39	70.5	13.6	622	2 Q6YB51	Q6YB51 mus musculu
40	70.5	13.6	622	2 Q8CEA0	Q8CEA0 mus musculu
41	70.5	13.6	622	2 Q8CFP1	Q8CFP1 mus musculu
42	70.5	13.6	622	2 AAQ24761	AAQ24761 mus muscu
43	70	13.5	1144	2 Q7PM73	Q7PM73 anopheles g
44	69.5	13.4	413	2 Q6JEK7	Q6JEK7 dasytus nov
45	69.5	13.4	413	2 AAH75798	AAH75798 dasytus n

ALIGNMENTS

RESULT 1
IRA4_HUMAN STANDARD; PRT; 460 AA.
ID IRA4_HUMAN
AC Q9NWZ3; Q8TDE7; Q9Y589;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.-) (IRAK-4) (NY-REN-64 antigen).
GN Name=IRAK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND INTERACTIONS WITH IRAK1 AND TRAF6.
RX MEDLINE=21957277; PubMed=11960013; DOI=10.1073/pnas.082100399;
RA Li S., Strelow A., Fontana E.J., Wesche H.;
RT "IRAK4: A novel member of the IRAK family with the properties of an
RT cell carcinoma."
RL Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99438124; PubMed=10508479;
RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,
RA Jongsomjit C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
RA Old L.J.;
RT "Antigens recognized by autologous antibody in patients with renal-
RT cell carcinoma."
RL Int. J. Cancer 83:456-464(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu N., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K.,
RA Yamazaki M., Niimiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori Y., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Mutsaers K., Komiya F., Oshima H., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RT Nat. Genet. 36:40-45(2004).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-98; ARG-390 AND THR-428.
 RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.,
 RT "SealSnpS: NIMBL HUG6662 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (NCBI-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Mansina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bomaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley K.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Schein J.E., Jones S.J.M., Marra M.A.,
 RA Scheraga A., Krawitz M.I., Skalska U., Smalins D.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Involved in IL1R-induced NF-kappa-B (NFKB) activation as
 CC well as the activation of mitogen-activated protein (MAP) kinase
 CC pathways. Phosphorylates IRAK1.
 CC -1- SUBUNIT: Interacts with TRAF6 and IRAK1.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL, AF445802; AAM15772.1; -;
 DR EMBL, AF155118; AAD42884.1; -;
 DR EMBL, AK000528; BAA91232.1; -;
 DR EMBL, AY186092; AAN75440.1; -;
 DR EMBL, BC013316; AAI13316.1; -;
 DR HSSP, O62838; ILUP.
 DR GeneW, HGNC:17967; IRAK4.
 DR MIM, 606883; -;
 DR InterPro, IPR000719; Prot_kinase.
 DR InterPro, IPR001245; Tyr_kinase.
 DR Pfam, PF00069; Pkinase, 1.
 DR PRINTS, PR00109; TYRKINASE.
 DR PRODOM, PD000001; Prot_kinase, 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE, PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
 KW ATP-binding; Polymorphism; Serine/threonine-protein kinase;

KW Transferase.
 FT DOMAIN 186 454 Protein kinase.
 FT NP_BIND 192 200 ATP (By similarity).
 FT BINDING 213 213 ATP (By similarity).
 FT ACT_SITE 311 311 Proton acceptor (By similarity).
 FT VARIANT 98 98 S -> R.
 FT VARIANT 390 390 /FTID=VAR_019354.
 FT VARIANT 428 428 H -> R.
 FT VARIANT 428 428 /FTID=VAR_019355.
 FT CONFLICT 81 81 A -> T.
 FT CONFLICT 432 432 V -> A (in Ref. 1).
 FT CONFLICT 437 437 L -> R (in Ref. 2).
 FT CONFLICT 444 444 R -> S (in Ref. 2).
 FT CONFLICT 451 451 Q -> H (in Ref. 2).
 SQ SEQUENCE 460 AA; 51529 MW; 6C8156ADP25FP81E CRC64;
 Query Match 100.0%; Score 517; DB 1; Length 460;
 Best Local Similarity 99.0%; Pred. No. 1,4e-49;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINVLGIKRLSDFDIDPQEGWKLAVALIKKPSGDRVYQFHIRRFEALLQTKSPPTS 60
 DB 9 TYVRCINVLGIKRLSDFDIDPQEGWKLAVALIKKPSGDRVYQFHIRRFEALLQTKSPPTS 68
 QY 61 ELLEFDGTCNCTVGDVLDLILQNEFFAPASILLDPVAVP 98
 DB 69 ELLEFDGTCNCTVGDVLDLILQNEFFAPASILLDPVAVP 106
 RESULT 2
 QY 0726A7 PRELIMINARY; PRT; 218 AA.
 AC 0726A7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-1 receptor associated kinase 4 mutant form 2.
 GN Name=IRAK4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Medvedev A.B., Lentschat A., Kuhns D.B., Blanco J.C.G., Salkowski C.,
 RA Zhang S., Arditi M., Gallin J.I., Vogel S.N.,
 RT "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
 RT Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
 RT Bacterial Infections.";
 RT J. Exp. Med. 0:0-0(2003).
 DR EMBL, AY283671; AAP57090.1; -;
 DR GO, GO:0016301; P-kinase activity; IEA.
 DR GO, GO:0004872; F-receptor activity; IEA.
 KW Kinase; Receptor.
 SQ SEQUENCE 218 AA; 24257 MW; B42D2896DACBDF9 CRC64;
 Query Match 99.2%; Score 513; DB 2; Length 218;
 Best Local Similarity 99.0%; Pred. No. 1.6e-49;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TYVRCINVLGIKRLSDFDIDPQEGWKLAVALIKKPSGDRVYQFHIRRFEALLQTKSPPTS 60
 DB 9 TYVRCINVLGIKRLSDFDIDPQEGWKLAVALIKKPSGDRVYQFHIRRFEALLQTKSPPTS 68
 QY 61 ELLEFDGTCNCTVGDVLDLILQNEFFAPASILLDPVAVP 98
 DB 69 ELLEFDGTCNCTVGDVLDLILQNEFFAPASILLDPVAVP 106
 RESULT 3
 QY 0726A8

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ID Q726A8 PRELIMINARY; PRT; 292 AA.
AC Q726A8
DT 01-OCT-2003 (TREMblrel. 25, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Interleukin-1 receptor associated kinase 4 mutant form 1.
GN Name=IRAK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Medvedev A.E., Lentschat A., Kuhns D.B., Blanco J.C.G., Salkowski C.,
RA Zhang S., Altieri M., Gallin J.I., Vogel S.N.;
RT "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
RT Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
RT Bacterial Infections.";
RL J. Exp. Med. 0:0-0(2003).
DR EMBL; AY283670; AAP57089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot. kinase.
DR Pfam; PF00069; Kinase; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase; Receptor.
SQ SEQUENCE 292 AA; 32704 MW; 58F1708A63BD3BES CRC64;

Query Match 99.2%; Score 513; DB 2; Length 292;
Best Local Similarity 99.0%; Pred. No. 2.3e-49;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TYVCLAVGLIRKISDFIDPQEGKKLAIVAKKSGGDRYVQFIRREFALLQTKSKPTS 60
Db 9 TYVCLAVGLIRKISDFIDPQEGKKLAIVAKKSGGDRYVQFIRREFALLQTKSKPTS 68

Qy 61 ELFPDGTCTCTGVDLVLDLQNEFPAPASILLPDVAVP 98
Db 69 ELFPDGTCTCTGVDLVLDLQNEFPAPASILLPDVAVP 106

RESULT 4
Q9D250 PRELIMINARY; PRT; 197 AA.
ID Q9D250
AC Q9D250;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched
DE library, clone:9330209D03 product:interleukin-1 receptor-associated
DE kinase 4.
GN Name=Irak4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";

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RL Nature 409:665-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA The PANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Suni M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK020397; BAB32090.2; -.
DR MGD; MGI:2182474; Irak4.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR01029; Death_1.
DR InterPro; IPR01029; Death_1.
DR Pfam; PF00531; Death; 1.
KW Kinase; Receptor.
SQ SEQUENCE 197 AA; 21695 MW; 142B61EB8A614898 CRC64;

Query Match 92.1%; Score 476; DB 2; Length 197;
Best Local Similarity 90.8%; Pred. No. 2.2e-45;
Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TYVCLAVGLIRKISDFIDPQEGKKLAIVAKKSGGDRYVQFIRREFALLQTKSKPTS 60
Db 9 TYVCLAVGLIRKISDFIDPQEGKKLAIVAKKSGGDRYVQFIRREFALLQTKSKPTS 68

Qy 61 ELFPDGTCTCTGVDLVLDLQNEFPAPASILLPDVAVP 98
Db 69 ELFPDGTCTCTGVDLVLDLQNEFPAPASILLPDVAVP 106

RESULT 5
IRAK_MOUSE

```

ID IRA4 MOUSE STANDARD; PRT; 459 AA.
 AC Q8R4K2; Q80WM1;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.-) (IRAK-4).
 GN Name:Irak4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=21957277; PubMed=11960013; DOI=10.1073/pnas.082100399;
 RT Li S., Streleow A., Fontana E.J., Wesche H.;
 RT "IRAK: A novel member of the IRAK family with the properties of an
 RT IRAK-kinase.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RT Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nkaido I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schindach C., Gojodori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousine S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazier K.S.,
 RA Gaasterland T., Gariboldi M., Ghiasi C., Godzik A., Gough J.,
 RA Grimmond S., Guinrich S., Hirokawa N., Jackson I.V., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard R., Lyons P.A.,
 RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Whitlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arkhava T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.024603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidl T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimmond J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,
 RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Involved in IL1R-induced NF-kappa-B (NFKB) activation as
 CC well as the activation of mitogen-activated protein (MAP) kinase
 CC pathways. Phosphorylates IRAK1 (By similarity).
 CC -1- SUBUNIT: Interacts with TRAF6 and IRAK1 (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF445803; AAM15773.1; -;
 DR EMBL; AK028837; BAC26146.1; -;
 DR EMBL; BC051676; AAH51676.1; -;
 DR HSSP; P36897; 11AS.
 DR MED; MGJ:2182474; Irak4.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; FALSE_NEG.
 DR ATP-binding; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 186 454
 FT NP_BIND 192 200 ATP (By similarity).
 FT BINDING 213 213 ATP (By similarity).
 FT ACT_SITE 311 311 Proton acceptor (By similarity).
 FT CONFLICT 321 321 K -> R (in Ref. 3).
 SQ SEQUENCE 459 AA; 50871 MW; FC1AD06983B7AAB CRC64;
 Query Match 92.1% Score 476; DB 1; Length 459;
 Best Local Similarity 90.8%; Pred. No. 6e-45;
 Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TYRCLANGVLRKISDFIDPQGWKLAIVAKPSGDRNQHRRFALLQTSKSPS 60
 DB 9 TYIRLVANGVLRKISDFIDPQGWKLAIVAKPSGDRNQHRRFALLQTSKSPC 68
 QY 61 ELIPDWGTTNCTGVLDVLLIQNEFPAPASILLPDVAVP 98
 DB 69 ELIPDWGTTNCTGVLDVLLVQIELFAPATILLPDVAVP 106
 RESULT 6
 Q7ZWV7 PRELIMINARY; PRT; 382 AA.
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Similar to interleukin-1 receptor-associated kinase 4.
 GN Name=zgc55553;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleton M., Soares M.B., Bonaldo M.F., Cavaletti T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalske U., Smalios D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marrs M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045381; AAH45381.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR01029; DEATH like.
DR InterPro; IPR01029; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF0069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding; Kinase; Receptor.
SQ SEQUENCE 382 AA; 41769 MW; 2FDPD6B572B4CB2B CRC64;

Query Match 55.5%; Score 287; DB 2; Length 382;
Best Local Similarity 53.7%; Pred. No. 1,4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKLSDFIDPQEGWKLVAIKKPSGDDRYNQFHIRREALLQTKSPPTS 60
DB 8 TPVKLRYSALRALADLDPQDTWRSIMADISRCGEBRYTQMHRREACVLAGKSPSTM 67
61 ELFPDMGTNCTVGDVLDLIONEFPAPASILLPD 95
68 ELFPDMGTSDCTVGDVLEILRHQLFAAVTVLLPD 102
DB

RESULT 7
Q6IWL3 PRELIMINARY; PRT; 483 AA.
AC Q6IWL3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-1 receptor-associated kinase 4.
GN Name=Itak4;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Phelan P.E., Iii, Mellon M.T., Kim C.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY616584; AAT37635.1; -
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR01029; DEATH like.
DR InterPro; IPR01029; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF0069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding; Kinase; Receptor.
SQ SEQUENCE 483 AA; 53708 MW; 5F0BDAC250561F7 CRC64;

Query Match 55.5%; Score 287; DB 2; Length 483;
Best Local Similarity 53.7%; Pred. No. 1,4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKLSDFIDPQEGWKLVAIKKPSGDDRYNQFHIRREALLQTKSPPTS 60
DB 8 TPVKLRYSALRALADLDPQDTWRSIMADISRCGEBRYTQMHRREACVLAGKSPSTM 67
61 ELFPDMGTNCTVGDVLDLIONEFPAPASILLPD 95
68 ELFPDMGTSDCTVGDVLEILRHQLFAAVTVLLPD 102
DB

RESULT 8
AAT37635 PRELIMINARY; PRT; 483 AA.
AC AAT37635;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-1 receptor-associated kinase 4.
GN IRAK4.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Phelan P.E., Iii, Mellon M.T., Kim C.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY616584; AAT37635.1; -
KM Kinase; Receptor.
SQ SEQUENCE 483 AA; 53708 MW; 5F0BDAC250561F7 CRC64;

Query Match 55.5%; Score 287; DB 2; Length 483;
Best Local Similarity 53.7%; Pred. No. 1,4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKLSDFIDPQEGWKLVAIKKPSGDDRYNQFHIRREALLQTKSPPTS 60
DB 8 TPVKLRYSALRALADLDPQDTWRSIMADISRCGEBRYTQMHRREACVLAGKSPSTM 67
61 ELFPDMGTNCTVGDVLDLIONEFPAPASILLPD 95
68 ELFPDMGTSDCTVGDVLEILRHQLFAAVTVLLPD 102
DB

RESULT 9
Q8CTU8 PRELIMINARY; PRT; 609 AA.
AC Q8CTU8;
Q8CTU8;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
 DE clone: C330013G03 product: similar to interleukin-1 receptor-associated
 DE kinase M, full insert sequence.
 OS Name=Irak3;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN R1 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN R2 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RN R3 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RN R4 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN R5 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Taishiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN R6 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK092210; BAC33612.1; -.
 DR MGI:1921164; Irak3.

DR GO: 0016301; P:kinase activity; IDA.
 DR GO: 0006468; P:protein amino acid phosphorylation; IDA.
 DR GO: 0007165; P:signal transduction; IDA.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR011029; DEATH_1like.
 DR InterPro: IPR011009; Kinase_1like.
 DR InterPro: IPR000719; Prot_kinase.
 DR Pfam: PF00531; Death; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 66425 MW; C8FB51065B2313C4 CRC64;
 Query Match 19.1%; Score 98.5; DB 2; Length 609;
 Best Local Similarity 31.5%; Pred. No. 0.036;
 Matches 23; Conservative 13; Mismatches 30; Indels 7; Gaps 1;
 QY 8 VGLIRLSDPFDIPQSGMKLAVAIKKPGDDRYNDFHRRPEALLQSGKSPSTLPDWG 67
 Db 25 LSELGCIIDSCDGLPKMGLARLSN-----SWDVRHLEKRYNGKSGSTRLLMSWA 77
 QY 68 TTNCIVGDIIVDL 80
 Db 78 QKNKRTIGDLLEVL 90
 RESULT 10
 Q8CE40 PRELIMINARY; PRT; 609 AA.
 AC Q8CE40; Q8K1S8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
 DE library, clone: 473246H23 product: similar to interleukin-1 receptor-
 DE associated kinase M, full insert sequence (IL-1 receptor-associated
 DE kinase M).
 GN Name=Irak3; Synonyms=Irak-M;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN R1 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN R2 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RN R3 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RN R4 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN R5 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Taishiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN R6 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK092210; BAC33612.1; -.
 DR MGI:1921164; Irak3.

RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imocani J., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=balb/c;
 RX MEDLINE=22050158; PubMed=12054681;
 RA Rosati O., Martin M.U.,
 RT "Cloning of murine IL-1 receptor-associated-kinase M.";
 RL Biochem. Biophys. Res. Commun. 293:1472-1477(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=balb/c;
 RA Rosati O.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK029057; BAC26270.1; -
 DR EMBL; AJ440757; CAD29448.2; -
 DR MGI; MGI:1921164; Irak3.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 68455 MW; A63E010C9F29D856 CRC64;
 Query Match 19.1%; Score 98.5; DB 2; Length 609;
 Best Local Similarity 31.5%; Pred. No. 0.036;
 Matches 23; Conservative 13; Mismatches 30; Indels 7; Gaps 1;
 QY 8 VGLIRKLSDFIDPQEGWKKLAIVAKKSGDDRNQVFIIRFALLQTKGKSPSTSLFDMG 67
 DB 25 LGEICGILDSGDLGKRGIAERLSN-----SWLDVRHIEKYVQCKSGTRRLMSWA 77
 QY 68 TTNCTGDLVDLL 80
 DB 78 QKNTTIDLLLEVL 90
 RESULT 11
 QY616 PRELIMINARY; PRT; 596 AA.
 DT 01-NOV-1999 (TIREMBLrel. 12, Created)
 DT 01-NOV-1999 (TIREMBLrel. 12, Last sequence update)
 DT 01-OCT-2004 (TIREMBLrel. 28, Last annotation update)
 DE IL-1 receptor-associated-kinase-M (Interleukin-1 receptor-associated
 kinase 3).
 GN Name=IRAK3;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99315891; PubMed=10383454;
 RX Wesche H., Gao X., Li X., Kirschling C.J., Stark G.R., Cao Z.,
 RT "IRAK-M is a novel member of the Pelle/interleukin-1 receptor-
 associated kinase (IRAK) family.";
 RL J. Biol. Chem. 274:19403-19410(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones; and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bata S.S., Iguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerth A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strauberg R.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strauberg R.,
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF113136; AAD40879.1; -
 DR EMBL; BC057880; AAH57880.1; -
 DR EMBL; BC069388; AAH59388.1; -
 DR EMBL; HGNC:17020; IRAK3.
 DR GO; GO:0004672; F:protein kinase activity; TKS.
 DR GO; GO:0004702; F:receptor signaling protein serine/threonine...; TKS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TKS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TKS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH like.
 DR InterPro; IPR011009; kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00531; Death_1.
 DR Pfam; PF00063; Kinase_1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EAD07E38BE CRC64;
 Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058;
 Matches 23; Conservative 12; Mismatches 31; Indels 7; Gaps 1;
 QY 8 VGLIRKLSDFIDPQEGWKKLAIVAKKSGDDRNQVFIIRFALLQTKGKSPSTSLFDMG 67
 DB 25 LGEICAVLDSGDLGKRGIAERLSN-----SWLDVRHIEKYVQCKSGTRRLMSWA 77
 QY 68 TTNCTGDLVDLL 80

Db 78 QKNKTTIGDLDLQVL 90

RESULT 12

AAH57800 PRELIMINARY; PRT; 596 AA.
 AC AAH57800;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Interleukin-1 receptor-associated kinase 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diachenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Brownstein M.J., Ueda T.B., Toshiyuki S., Abramson R.D., Mullan S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057800; AAH57800.1; -.
 KW kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EAD7E38BE CRC64;

Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058; Indels 7; Gaps 1;
 Matches 23; Conservative 12; Mismatches 31;
 QY 8 VGLIRKLSDFIDPQEGWKKLVAIAIKKPSGDDRYNQFHIREALLQTKSPTSLFDWG 67
 DB 25 LGEICAVLDSGCGALGWRGLAERLSS-----SWLDVRHIEKYVDGKSGTRELMSWA 77
 QY 68 TTNCTVGDIVDLL 80
 DB 78 QKNKTTIGDLDLQVL 90

RESULT 13

AAH69388 PRELIMINARY; PRT; 596 AA.
 AC AAH69388;
 DT 20-MAY-2004 (TREMBlrel. 27, Created)
 DT 20-MAY-2004 (TREMBlrel. 27, Last sequence update)
 DE Interleukin-1 receptor-associated kinase 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]

RN SEQUENCE FROM N.A.
 RP TISSUE=PCR rescued clones;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diachenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Brownstein M.J., Ueda T.B., Toshiyuki S., Abramson R.D., Mullan S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=PCR rescued clones;
 RC Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069388; AAH69388.1; -.
 KW kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EAD7E38BE CRC64;

Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058; Indels 7; Gaps 1;
 Matches 23; Conservative 12; Mismatches 31;
 QY 8 VGLIRKLSDFIDPQEGWKKLVAIAIKKPSGDDRYNQFHIREALLQTKSPTSLFDWG 67
 DB 25 LGEICAVLDSGCGALGWRGLAERLSS-----SWLDVRHIEKYVDGKSGTRELMSWA 77
 QY 68 TTNCTVGDIVDLL 80
 DB 78 QKNKTTIGDLDLQVL 90

RESULT 14

Q8K4B2 PRELIMINARY; PRT; 609 AA.
 AC Q8K4B2;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Interleukin-1 receptor-associated kinase M.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6;
 RC MEDLINE=22150927; PubMed=12150927;
 RA Kobayashi K., Hernandez L.D., Galan J.E., Janeway C.A. Jr., Medzhitov R., Flavell R.A.;
 "IRAK-M is a negative regulator of Toll-like receptor signaling";
 Cell 110:191-202(2002).
 RL EMBL; AF461763; AAH83393.1; -.
 DR MGD; MGI:1921164; Irak3.
 GO; GO:0016301; P:kinase activity; IRA.
 GO; GO:0006468; P:protein amino acid phosphorylation; IRA.

DR GO:0007165; P:signal transduction; IDA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 68657 MW; 19BAD129F854DD73 CRC64;

Query Match 18.4%; Score 95; DB 2; Length 609;
 Best Local Similarity 32.4%; Pred. No. 0.089;
 Matches 24; Conservative 12; Mismatches 28; Indels 10; Gaps 2;

QY 10 LIRKLSDFIDPQ---GKKLAVAIKKPSGDDRYNQFHIRFEALLQTGKSPTSSELPDW 66
 DB 24 LIGELCGILDSWDGPIGWWGLAERLSN-----SWLDVRIEIKYKNGKSGTRELLEMSW 76
 QY 67 GTTNCYVGDLVDLL 80
 DB 77 AQKKNKTIGDLLEVL 90

RESULT 15

06Y1S1 PRELIMINARY; PRT; 296 AA.
 AC 06Y1S1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Myeloid differentiation primary response gene 88.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar; TISSUE=Spleen;
 RA Li Y., Ji A., Schaffer M.K.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY191270; AAC91937.1; -
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF01582; TIR; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR SEQUENCE 296 AA; 33883 MW; 7A74304BE61DBC80 CRC64;

Query Match 17.0%; Score 88; DB 2; Length 296;
 Best Local Similarity 35.0%; Pred. No. 0.23;
 Matches 28; Conservative 11; Mismatches 25; Indels 16; Gaps 4;

QY 6 LNYGLIRKLSDFIDPQ---EGWKLAVAIKKPSGDDRYNQFHIRFEALLQTGKSPTSSE 61
 DB 25 LNWGVRRRLSLFLNPRFTAAADWTSLEEM-----GFVLEIRFE---TRPDPTRS 73
 QY 62 LLFDW-GTTNCTYVGDLVDLL 80
 DB 74 LLDAMQGRSGSSVGRLELLEL 93

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	100.0	206	US-09-166-350-21	Sequence 21, Appli
2	96.5	18.7	596	US-09-135-232-2	Sequence 2, Appli
3	96.5	18.7	596	US-09-863-549-2	Sequence 2, Appli
4	79	15.3	590	US-08-980-060-2	Sequence 2, Appli
5	79	15.3	590	US-09-307-185-2	Sequence 2, Appli
6	79	15.3	590	US-09-773-753-2	Sequence 2, Appli
7	79	15.3	625	US-08-980-060-4	Sequence 4, Appli
8	79	15.3	625	US-09-307-185-4	Sequence 4, Appli
9	79	15.3	625	US-09-773-753-4	Sequence 4, Appli
10	69.5	13.4	398	US-09-360-545-20	Sequence 20, Appli
11	69.5	13.4	593	US-09-234-393-24	Sequence 24, Appli
12	69.5	13.4	593	US-09-234-393-50	Sequence 50, Appli
13	69.5	13.4	593	US-09-234-393-52	Sequence 52, Appli
14	69.5	13.4	593	US-09-234-393-54	Sequence 54, Appli
15	69.5	13.4	593	US-09-865-171-24	Sequence 24, Appli
16	69.5	13.4	593	US-09-865-171-50	Sequence 50, Appli
17	69.5	13.4	593	US-09-865-171-52	Sequence 52, Appli
18	69.5	13.4	593	US-09-865-171-54	Sequence 54, Appli
19	69.5	13.4	593	US-09-398-395A-50	Sequence 50, Appli
20	69.5	13.4	593	US-09-887-586A-50	Sequence 50, Appli
21	69.5	13.4	593	US-09-895-752-50	Sequence 50, Appli
22	69.5	13.4	593	US-09-903-012B-50	Sequence 50, Appli
23	69.5	13.4	593	US-09-900-797-50	Sequence 50, Appli
24	66.5	12.9	215	US-09-489-039A-12848	Sequence 12848, A
25	66	12.8	70	US-09-248-796A-21148	Sequence 21148, A
26	66	12.8	328	US-09-252-991A-27822	Sequence 27822, A
27	64.5	12.5	506	US-09-134-001C-3307	Sequence 3307, Ap

28	64.5	12.5	662	US-09-534-228B-2	Sequence 2, Appli
29	63.5	12.3	501	US-08-980-060-6	Sequence 6, Appli
30	63.5	12.3	501	US-09-307-185-6	Sequence 6, Appli
31	63.5	12.3	501	US-09-773-753-6	Sequence 6, Appli
32	63	12.1	430	US-09-489-039A-7580	Sequence 7580, Ap
33	62.5	12.1	125	US-09-543-681A-7171	Sequence 7171, Ap
34	62.5	12.1	499	US-09-543-681A-6427	Sequence 6427, Ap
35	62.5	12.1	520	US-09-724-623-124	Sequence 124, App
36	62.5	12.1	680	US-09-248-796A-16453	Sequence 16453, A
37	62.5	12.1	1423	US-08-810-712-10	Sequence 10, Appli
38	62.5	12.1	1431	US-09-538-092-1198	Sequence 1198, Ap
39	62.5	12.1	1674	US-08-968-542C-12	Sequence 12, Appli
40	62.5	12.1	1674	US-09-554-467A-12	Sequence 12, Appli
41	62	12.0	428	US-09-608-285A-7	Sequence 7, Appli
42	62	12.0	428	US-09-608-285A-7	Sequence 7, Appli
43	62	12.0	428	US-09-370-265-7	Sequence 7, Appli
44	62	12.0	428	US-09-357-800C-7	Sequence 7, Appli
45	62	12.0	428	US-09-370-625A-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
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; Sequence 21, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scania, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: 10461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-21
Query Match          100.0%; Score 517; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.7e-64;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYVCLANGLIRKLSDFIDPQGWKLAVALIKKPSGDRVYQFIHRRFALLQTKSPTS 60
DB 9 TYVCLANGLIRKLSDFIDPQGWKLAVALIKKPSGDRVYQFIHRRFALLQTKSPTS 68
QY 61 ELFPDWGTTCTVGDVLDLIIQNEFPAPASLLPDVAVP 98
DB 69 ELFPDWGTTCTVGDVLDLIIQNEFPAPASLLPDVAVP 106
RESULT 2
US-09-135-232-2
; Sequence 2, Application US/09135232
; Patent No. 6262228
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: 798-019
; CURRENT APPLICATION NUMBER: US/09/135,232
; CURRENT FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/980,060
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: STEEFE, ERIC K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
/ US-09-773-753-4

Query Match 15.3%; Score 79; DB 4; Length 625;
Best Local Similarity 31.1%; Pred. No. 0.056;
Matches 22; Conservative 12; Mismatches 19; Indels 16; Gaps 2

QY 45 IRREPEALQGT-GKSPTELLFDWGTCTTCTGVDLVLLIQLONEFFAPASLLT----- 93
Db 42 IIRIKEMERQGVSIITRELLMMWGMKRAVQGLVDLLCRLEIVRAQIILNWKPAPEINC 101
QY 94 -----PDAY 97
Db 102 PIPAPPSV 110

RESULT 10
US-09-360-545-20
/ Sequence 20, Application US/09360545
/ Patent No. 6428014
/ GENERAL INFORMATION:
/ APPLICANT: Croteau, Rodney B
/ APPLICANT: Bohlmann, Jorg
/ APPLICANT: Steele, Christopher L
/ APPLICANT: Phillips, Michael A
/ TITLE OR INVENTION: MONOTRYPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
/ FILE REFERENCE: wslu13885
/ CURRENT APPLICATION NUMBER: US/09/360,545
/ CURRENT FILING DATE: 1999-07-26
/ EARLIER APPLICATION NUMBER: 60/052,249
/ EARLIER FILING DATE: 1997-11-07
/ EARLIER APPLICATION NUMBER: PCT/US98/14528
/ EARLIER FILING DATE: 1998-07-10
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Abies grandis
/ US-09-360-545-20

Query Match 13.4%; Score 69.5; DB 4; Length 398;
Best Local Similarity 31.1%; Pred. No. 0.62;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

QY 3 VQCLNVGLIRKLSDFID-POEGWKK-----LAVAIRKPSGDD-----RYNOFHIRPEAL 51
Db 167 VRRWVDSLVGEGJPFMEKIAFEFMIKTSNELIAEAV-KAGQOMAAVIRKNAME-RYLEAY 224
QY 52 LG-----TGKSPTELLFDWGTCTN---CTVGDVLLIQLONE-----FFAP----- 88
Db 225 LQDAWIRATGVVPTFDEYLVNNGIPNIGMCVL-NLIPILLMGSHLPDILEQIFLPSRPH 283
QY 89 -----ASLLPDA 96
Db 284 LTELASRLVDVA 295

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Query Match	13.4%	Score 69.5	DB 3	Length 593
Best Local Similarity	31.1%	Pred. No. 1.1		
Matches 41; Conservative	13	Mismatches	37	Indels 41; Gaps 10;

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Db      362 VRKRDVSLVEGEPDPMKTAIEFEFWLTSNELLAEEA-KQGGOMAAIYIRKNAME-YYLEAY  419

QY      52 LQ-----TGKPSSELLFDWGTTN---CTWGDLVDLLIONE-----FFAP-----  88
Db      420 LQDAEWLNTGTVPTFDEYLNNGTPTNGCVL-NLPLPLMGSHPLDILEQIFLPSRHH  478

QY      89 ----ASLLLPDA  96
Db      479 LIELASRLVDDA  490

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RESULT 12
US-09-234-393-50
Sequence 50, Application US/09234393A
Patent No. 6265639
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: NSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 593
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(617)
OTHER INFORMATION: Computer-generated protein sequence

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RESULT 13
US-09-234-393-52
; Sequence 52, Application US/09234393A

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? APPLICANT: Crock, John E
? APPLICANT: Bohlman, Jorg
? APPLICANT: Jetter, Reinhard
? APPLICANT: Steele, Christopher L
? TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
? TITLE OF INVENTION: AND METHODS OF USE
? FILE REFERENCE: MSUR11345
? CURRENT APPLICATION NUMBER: US/09/234,393A
? CURRENT FILING DATE: 1999-01-20
? EARLIER APPLICATION NUMBER: 60/072,204
? EARLIER FILING DATE: 1998-01-22
? NUMBER OF SEQ ID NOS: 55
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 52
? LENGTH: 593
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: Description of Artificial Sequence:
? OTHER INFORMATION: protein
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)..(617)
? OTHER INFORMATION: Computer-generated protein sequence
? OS-09-234-393-52

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[illegible]

RESULT 14
US-09-234-393-54
; Sequence 54, Application US/09234393A
; Patent No. 6265639
; GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: MSUR11345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 593
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: protein
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(817)
OTHER INFORMATION: Computer-generated protein sequence
US-09-234-393-54

Query Match 13.4%; Score 69.5; DB 3; Length 593;
Best Local Similarity 31.1%; Pred. No. 1.1;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

QY 3 VRCLNVGLIRKLSDFID-POEGWK-----LAVAIIKPSGDD-----RYNQFHIRRREAL 51
DB 362 VARMVSLVEGLPDPFKIAFEFWLKTNSNELIABAV-KAOGODMAVYIRKNAME-RYLEAY 419
QY 52 IQ-----TKSPISSELLFDWGTTN---CTVGDVLDLLIONE-----FFAP----- 88
DB 420 LODAEWIAIGHVPTDEYILNNGTPNTGMCVL-NILPILMGHEHLPIDILEQIFLPSRFHH 478
QY 89 ----ASLLLPDA 96
DB 479 LIELASRLVDDA 490

RESULT 15
US-09-865-171-24
Sequence 24, Application US/09865171
Patent No. 6451576
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: MSUR117468
CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/234,393
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/072,204
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 593
TYPE: PRT
ORGANISM: Abies grandis
US-09-865-171-24

Query Match 13.4%; Score 69.5; DB 4; Length 593;
Best Local Similarity 31.1%; Pred. No. 1.1;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

QY 3 VRCLNVGLIRKLSDFID-POEGWK-----LAVAIIKPSGDD-----RYNQFHIRRREAL 51
DB 362 VARMVSLVEGLPDPFKIAFEFWLKTNSNELIABAV-KAOGODMAVYIRKNAME-RYLEAY 419
QY 52 IQ-----TKSPISSELLFDWGTTN---CTVGDVLDLLIONE-----FFAP----- 88
DB 420 LODAEWIAIGHVPTDEYILNNGTPNTGMCVL-NILPILMGHEHLPIDILEQIFLPSRFHH 478
QY 89 ----ASLLLPDA 96
DB 479 LIELASRLVDDA 490

Search completed: January 10, 2005, 23:26:36
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 23:25:15 ; Search time 145 Seconds
(without alignments)
243.696 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
Sequence: 1 TYVRCIANGVGLIRKLSDFIDP.....LLIIONEFAPASILLPDAVP 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_Aa:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	98	14	US-10-001-254-6
2	517	100.0	460	14	US-10-001-254-16
3	517	100.0	460	14	US-10-001-254-28
4	513	99.2	460	9	US-09-795-595-1
5	513	99.2	460	10	US-09-759-595-1
6	476	92.1	459	9	US-09-795-595-3
7	476	92.1	459	10	US-09-759-595-3
8	247	47.8	59	14	US-10-001-254-26
9	96.5	18.7	596	9	US-09-863-549-2
10	96.5	18.7	644	15	US-10-425-114-54258
11	95	18.4	609	14	US-10-340-545-2
12	79	15.3	590	9	US-09-773-753-2
13	79	15.3	590	14	US-10-366-288-20

14	79	15.3	590	16	US-10-657-146-2	Sequence 2, Appl1
15	79	15.3	625	9	US-09-773-753-4	Sequence 4, Appl1
16	79	15.3	625	16	US-10-657-146-4	Sequence 4, Appl1
17	72.5	14.0	824	14	US-10-024-298A-131	Sequence 131, App
18	72.5	14.0	824	14	US-10-042-211A-131	Sequence 131, App
19	72.5	14.0	824	15	US-10-617-217A-131	Sequence 131, App
20	72.5	14.0	824	17	US-10-024-298A-131	Sequence 131, App
21	72.5	14.0	928	16	US-10-437-963-152971	Sequence 152971, App
22	71.5	13.8	5836	15	US-10-378-083-20	Sequence 23, Appl1
23	71	13.7	259	9	US-09-987-107-23	Sequence 23, Appl1
24	71	13.7	259	14	US-10-316-253-277	Sequence 277, App
25	71	13.7	259	14	US-10-316-253-285	Sequence 285, App
26	71	13.7	259	14	US-10-316-253-287	Sequence 287, App
27	71	13.7	259	14	US-10-316-253-289	Sequence 289, App
28	69.5	13.4	398	14	US-10-025-145A-20	Sequence 20, Appl1
29	69.5	13.4	593	9	US-09-865-171-24	Sequence 24, Appl1
30	69.5	13.4	593	9	US-09-865-171-50	Sequence 50, Appl1
31	69.5	13.4	593	9	US-09-865-171-52	Sequence 52, Appl1
32	69.5	13.4	593	9	US-09-865-171-54	Sequence 54, Appl1
33	69.5	13.4	593	9	US-09-895-752-50	Sequence 50, Appl1
34	69.5	13.4	593	9	US-09-887-586A-50	Sequence 50, Appl1
35	69.5	13.4	593	9	US-09-903-012-50	Sequence 50, Appl1
36	69.5	13.4	593	10	US-09-900-797-50	Sequence 50, Appl1
37	69.5	13.4	593	11	US-09-893-820-50	Sequence 50, Appl1
38	69.5	13.4	593	13	US-10-041-007-20	Sequence 20, Appl1
39	68.5	13.2	964	16	US-10-437-963-119980	Sequence 119980, App
40	67.5	13.1	413	16	US-10-437-963-186825	Sequence 186825, App
41	67.5	13.1	527	9	US-09-815-242-11374	Sequence 11374, A
42	67.5	13.1	527	15	US-10-282-122A-58815	Sequence 58815, A
43	67.5	13.1	733	16	US-10-437-963-142702	Sequence 142702, App
44	67.5	13.1	813	16	US-10-437-963-142703	Sequence 142703, App
45	67.5	13.1	813	16	US-10-437-963-186828	Sequence 186828, App

ALIGNMENTS

RESULT 1
US-10-001-254-6
Sequence 6, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Steiner-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-1J 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-6

Query Match 100.0%; Score 517; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TYVRCIANGVGLIRKLSDFIDPQEGWKLVAIAIKKSGSDRYNQFIIRFEALLQTKSPTS 60
1 TYVRCIANGVGLIRKLSDFIDPQEGWKLVAIAIKKSGSDRYNQFIIRFEALLQTKSPTS 60

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QY 61 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 61 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 98

RESULT 2
US-10-001-254-16
; Sequence 16, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stemmer-Liewen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-16

Query Match 100.0%; Score 517; DB 14; Length 460;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 60
DB 9 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 69 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 3
US-10-001-254-28
; Sequence 28, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stemmer-Liewen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-28
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Query Match 100.0%; Score 517; DB 14; Length 460;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 60
DB 9 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 69 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 4
US-09-795-595-1
; Sequence 1, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/795,595
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-595-1

Query Match 99.2%; Score 513; DB 9; Length 460;
Best Local Similarity 99.0%; Pred. No. 1.1e-55;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 60
DB 9 TYVRCINVLIRKLSDFIDPQEGWKLAVAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 69 ELFPDGTGTCVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 5
US-09-759-595-1
; Sequence 1, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-595-1

Query Match 99.2%; Score 513; DB 10; Length 460;
Best Local Similarity 99.0%; Pred. No. 1.1e-55;
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Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 60
Db 9 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

Qy 61 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 98
Db 69 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 106

RESULT 6
US-09-795-595-3

; Sequence 3, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/795,595
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-795-595-3

Query Match 92.1%; Score 476; DB 9; Length 459;
Best Local Similarity 90.8%; Pred. No. 4.9e-51;
Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 9 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

Qy 61 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 98
Db 69 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 106

RESULT 7
US-09-759-595-3

; Sequence 3, Application US/09759595
; Publication No. US2003005916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; CURRENT FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-759-595-3

Query Match 92.1%; Score 476; DB 10; Length 459;
Best Local Similarity 90.8%; Pred. No. 4.9e-51;
Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 60

Db 9 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

Qy 61 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 98
Db 69 ELFPDGTCTGVDLVDLLIQNEFPAPASLLPDAPV 106

RESULT 8
US-10-001-254-26

; Sequence 26, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Steiner-Jewen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-26

Query Match 47.8%; Score 247; DB 14; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.9e-23;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 46
Db 9 TYVCLNVLGRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 54

RESULT 9
US-09-863-549-2

; Sequence 2, Application US/09863549
; Patent No. US20020049300A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: 798-019
; CURRENT APPLICATION NUMBER: US/09/863,549
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/135,232
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 596
; TYPE: PRT
; ORGANISM: human
US-09-863-549-2

Query Match 18.7%; Score 96.5; DB 9; Length 596;
Best Local Similarity 31.5%; Pred. No. 0.0056;
Matches 23; Conservative 12; Mismatches 31; Indels 7; Gaps 1;

Qy 8 VGLIRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHRRFEALLQTKSPTS 67
Db 25 LGEICAVLSDCDGALGWRGLAERLS-----SWLDVRIEYKVDGSGGTREILMSWA 77

Matches	22;	Conservative	12;	Mismatches	19;	Indels	16;	Gaps	2;
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Qy	94	-----PDAV 97							
Db	102	PIPAFPDSV 110							

Search completed: January 10, 2005, 23:37:31
 Job time : 146 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 08:09:24 ; Search time 465 Seconds

(without alignments)
1210.961 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database :

Published Applications NA.*
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11: /cgnt_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	294	14 US-10-001-254-5	Sequence 5, Appl1
2	517	100.0	1383	14 US-10-001-254-15	Sequence 15, Appl1
3	517	100.0	2817	10 US-09-966-451-3	Sequence 3, Appl1
4	517	100.0	2817	14 US-10-001-254-27	Sequence 27, Appl1
5	517	100.0	2817	16 US-10-630-399-3	Sequence 3, Appl1
6	513	99.2	1383	9 US-09-795-595-2	Sequence 2, Appl1
7	513	99.2	1383	10 US-09-759-595-2	Sequence 4, Appl1
8	476	92.1	1542	9 US-09-759-595-4	Sequence 4, Appl1
9	476	92.1	1542	10 US-09-759-595-4	Sequence 149, Appl1
10	413	79.9	501	9 US-09-833-790-149	Sequence 10, Appl1
11	256	49.5	31000	16 US-10-966-451-10	Sequence 10, Appl1
12	256	49.5	31000	16 US-10-630-399-10	Sequence 25, Appl1
13	247	47.8	211	14 US-10-001-254-25	Sequence 26096, A
14	247	47.8	470	16 US-10-242-535A-26096	Sequence 26096, A
15	247	47.8	470	16 US-10-085-783A-26096	Sequence 428, App
16	134.5	26.0	408	11 US-09-969-034-428	Sequence 1, Appl1
17	96.5	18.7	2288	9 US-09-863-549-1	Sequence 3, Appl1
18	96.5	18.7	2292	13 US-10-098-841-3	Sequence 26259, A
19	96.5	18.7	2406	16 US-10-425-114-26259	Sequence 1, Appl1
20	95	18.4	1888	15 US-10-340-545-1	Sequence 1432, Appl1
21	79.5	15.4	476	14 US-10-198-846-1432	Sequence 19, Appl1
22	79	15.3	1782	15 US-10-366-288-19	Sequence 1, Appl1
23	79	15.3	1806	9 US-09-773-753-1	Sequence 1, Appl1
24	79	15.3	1806	17 US-10-657-146-1	Sequence 3, Appl1
25	79	15.3	3459	9 US-09-773-753-3	Sequence 3, Appl1
26	79	15.3	3459	17 US-10-657-146-3	Sequence 14, Appl1
27	78.5	15.2	479	17 US-10-657-146-14	Sequence 384, App
28	78.5	15.2	708	16 US-10-424-599-384	Sequence 3589, App
29	78.5	15.2	861	9 US-09-764-877-3589	Sequence 3587, App
30	78.5	15.2	861	16 US-10-242-515-3589	Sequence 3587, App
31	78.5	15.2	864	9 US-09-764-877-3587	Sequence 3587, App
32	78.5	15.2	864	9 US-09-764-877-3590	Sequence 3590, App
33	78.5	15.2	864	16 US-10-242-515-3590	Sequence 1011, App
34	78.5	15.2	864	16 US-10-242-515-3590	Sequence 83917, A
35	78.5	15.2	3128	9 US-10-108-260A-759	Sequence 50723, A
36	74.5	14.6	774	6 US-09-974-300-1011	Sequence 50723, A
37	74.5	14.4	1153	17 US-10-437-963-83917	Sequence 50723, A
38	73.5	14.2	1153	17 US-10-027-632-50723	Sequence 50723, A
39	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
40	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
41	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
42	73	14.1	497	15 US-10-027-632-50724	Sequence 72567, A
43	73	14.1	499	13 US-10-027-632-72567	Sequence 72567, A
44	73	14.1	499	13 US-10-027-632-72568	Sequence 72568, A
45	73	14.1	499	15 US-10-027-632-72567	Sequence 72567, A

ALIGNMENTS

RESULT 1
US-10-001-254-5
Sequence 5, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfried
APPLICANT: Steiner-Liwen, Frank
TITLE OF INVENTION: P-1J 5037
FILE REFERENCE: No. US20030049702A1e1 Death Domain Proteins
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/10/001,254
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 294
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (294)
US-10-001-254-5

Alignment Scores:

Pred. No.:	2,696-71	Length:	294
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-001-254-6 (1-98) x US-10-001-254-5 (1-294)

QY 1 ThTyrValArgCysLeuAnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 1 ACATATGTGGCTGCTCAATGTGGACTAATTGGAAGCTGTCAATTTTATTGATCCT 60
QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 61 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGGTGATGATGATAC 120
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 121 AATCATGTTTCACATTAAGAGATTTGAGCACTTCTTAACCTGAAAAAGTCCCACTTCT 180
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 181 GAATTACTGTTTGACTGGGGCACCAAAATTGCACGTTGTGATCTTGTGATCTTTTG 240
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 241 ATCCAAATGAAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 294

RESULT 2

US-10-001-254-15
Sequence 15, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sung Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Stemmer-Ulrich, Frank
TITLE OF INVENTION: No. US20030049702A1: Death Domain Proteins
FILE REFERENCE: P-Lt 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (1380)
US-10-001-254-15

Alignment Scores:

Pred. No.:	2,486-70	Length:	1383
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Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-001-254-6 (1-98) x US-10-001-254-15 (1-1383)

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DB 25 ACATATGTGGCTGCTCAATGTGGACTAATTGGAAGCTGTCAATTTTATTGATCCT 84
QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 85 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGGTGATGATGATAC 144
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 145 AATCATGTTTCACATTAAGAGATTTGAGCACTTCTTAACCTGAAAAAGTCCCACTTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCAAAATTGCACAGTGGTGATCTTGTGATCTTTTG 264
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 318

RESULT 3

US-09-966-451-3
Sequence 3, Application US/09966451
Publication No. US20030087856A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freiler
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 (EXPRESS)
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50) ... (1432)
US-09-966-451-3

Alignment Scores:

Pred. No.:	6,876-70	Length:	2817
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-001-254-6 (1-98) x US-09-966-451-3 (1-2817)

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DB 74 ACATATGTGGCTGCTCAATGTGGACTAATTGGAAGCTGTCAATTTTATTGATCCT 133
QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 134 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGGTGATGATGATAC 193
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 194 AATCATGTTTCACATTAAGAGATTTGAGCACTTCTCAAACTGAAAAAGTCCCACTTCT 253
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

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Db      254 GAATTACTGTTGACGGGGGACCAAAATGACAGTTGGATCTTGATCTTTTG 313
Qy      81 116G1nang1uphephea1aPro1aSer1eu1euP1roaSp1aVal1Pro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 4
US-10-001-254-27
; Sequence 27, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawloweki, Krzysztof
; APPLICANT: Fiorentino, Loreana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenner-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-1J 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1429)
; US-10-001-254-27

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Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x US-10-001-254-27 (1-2817)
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Db      134 CAAGAAGATGGAAGAGTGTAGCTGTACTATTAAAAAACCATCTGGTGATGATGATAC 193
Qy      41 AsnGlnPheHis1leArgArgPheGluAlaLeuLeuGlnThrGlyLySleProThSer 60
Db      194 AATAGATTTCACATAGAGATTGAGACATTACTTCAACTGGAAGAAAAGTCCCACTTCT 253
Qy      61 GluLeuLeuPheAppTPpGlyThrThrasnCysThrValGlyAspLeuValAspLeuLeu 80
Db      254 GAATTACTGTTGACGGGGGACCAAAATGACAGTTGGATCTTGATCTTTTG 313
Qy      81 116G1nang1uphephea1aPro1aSer1eu1euP1roaSp1aVal1Pro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 5
US-10-630-399-3
; Sequence 3, Application US/10630399
; Publication No. US20040019009A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett

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; APPLICANT: Susan M. Freter
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RRS-0324
; CURRENT APPLICATION NUMBER: US/10/630,399
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1432)
; US-10-630-399-3

Alignment Scores:
Pred. No.: 6.87e-70 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db      74 ACATATGCGCGCTCCTCAATGTTGACTAATTAGAAAGCTGTGATTTTATGATCCT 133
Qy      21 G1nG1nG1yTPpLySlyLeuAlaValAla1leLySlyProSeG1yAspAspArgTy 40
Db      134 CAAGAAGATGGAAGAGTGTAGCTGTACTATTAAAAAACCATCTGGTGATGATGATAC 193
Qy      41 AsnGlnPheHis1leArgArgPheGluAlaLeuLeuGlnThrGlyLySleProThSer 60
Db      194 AATAGATTTCACATAGAGATTGAGACATTACTTCAACTGGAAGAAAAGTCCCACTTCT 253
Qy      61 GluLeuLeuPheAppTPpGlyThrThrasnCysThrValGlyAspLeuValAspLeuLeu 80
Db      254 GAATTACTGTTGACGGGGGACCAAAATGACAGTTGGATCTTGATCTTTTG 313
Qy      81 116G1nang1uphephea1aPro1aSer1eu1euP1roaSp1aVal1Pro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 6
US-09-795-595-2
; Sequence 2, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/795,595
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; OTHER INFORMATION: CDNA
; NAME/KEY: CDS
; LOCATION: (1) ... (1383)
; OTHER INFORMATION: human IRAK-4

```

US-09-795-595-2

Alignment Scores:

Pred. No.:	1.05e-69	Length:	1383
Score:	513.00	Matches:	97
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	9	Gaps:	0

US-10-001-254-6 (1-98) x US-09-795-595-2 (1-1383)

Qy 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
Db 25 ACATATGTCGCGCTCAATGTTGAGCTAATTAGGAAGCTGTCCAGATTTTATGATCCT 84
Qy 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 85 CAAGAAGATGGAGAAGATTAGCTAGCTATTAAAAACCATCTGTGTGATGATGATAC 144
Qy 41 AengInPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 145 AATCAGTTTCACATAGAGAGATTGAGCACTTCTCAACCTGCAAAAAGTCCCACTTCT 204
Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 205 GAATTAAGTCTTGGACTGGGGCACCAAAATTGCACAGCTGTGATCTTGTGGATCTTTTG 264
Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 265 ATCCAAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTCC 318

RESULT 7

US-09-759-595-2
; Sequence 2, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-09-759-595-2

Alignment Scores:

Pred. No.:	1.05e-69	Length:	1383
Score:	513.00	Matches:	97
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	10	Gaps:	0

US-10-001-254-6 (1-98) x US-09-759-595-2 (1-1383)

Qy 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
Db 25 ACATATGTCGCGCTCAATGTTGAGCTAATTAGGAAGCTGTCCAGATTTTATGATCCT 84
Qy 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 85 CAAGAAGATGGAGAAGATTAGCTAGCTATTAAAAACCATCTGTGTGATGATGATAC 144
Qy 41 AengInPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 145 AATCAGTTTCACATAGAGAGATTGAGCACTTCTCAACCTGCAAAAAGTCCCACTTCT 204
Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 205 GAATTAAGTCTTGGACTGGGGCACCAAAATTGCACAGCTGTGATCTTGTGGATCTTTTG 264
Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 265 ATCCAAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTCC 318

Db 25 ACATATGTCGCGCTCAATGTTGAGCTAATTAGGAAGCTGTCCAGATTTTATGATCCT 84

Qy 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40

Db 85 CAAGAAGATGGAGAAGATTAGCTAGCTATTAAAAACCATCTGTGTGATGATGATAC 144

Qy 41 AengInPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60

Db 145 AATCAGTTTCACATAGAGAGATTGAGCACTTCTCAACCTGCAAAAAGTCCCACTTCT 204

Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80

Db 205 GAATTAAGTCTTGGACTGGGGCACCAAAATTGCACAGCTGTGATCTTGTGGATCTTTTG 264

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

Db 265 ATCCAAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTCC 318

RESULT 8

US-09-795-595-4
; Sequence 4, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
US-09-795-595-4

Alignment Scores:

Pred. No.:	7.87e-64	Length:	1542
Score:	476.00	Matches:	89
Percent Similarity:	95.92%	Conservative:	5
Best Local Similarity:	90.82%	Mismatches:	4
Query Match:	92.07%	Indels:	0
DB:	9	Gaps:	0

US-10-001-254-6 (1-98) x US-09-795-595-4 (1-1542)

Qy 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
Db 187 ACATATGTCGCGCTCAATGTTGAGCTAATTAGGAAGCTGTCCAGATTTTATGATCCT 246
Qy 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 247 CAAGAAGATGGAGAAGATTAGCTAGCTATTAAAAAGCGTCCGGGACAGACAGATAC 306
Qy 41 AengInPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 307 AATCAGTTTCACATAGAGAGATTGAGCACTTCTCAACCTGCAAAAAGTCCCACTTCT 366
Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 367 GAATTAAGTCTTGGACTGGGGCACCAAAATTGCACAGCTGTGATCTTGTGGATCTTTTG 426
Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

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Db      427 GTCCAGATTGAGCTGTTGGCCCGGCACCTCTCCGTGGCGGAGATGCCGTTCCC 480
      RESULT 9
      US-09-759-595-4
      ; Sequence 4, Application US/09759595
      ; Publication No. US20030059916A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Weeche, Holger
      ; APPLICANT: Li, Shyun
      ; APPLICANT: Tularik Inc.
      ; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
      ; FILE REFERENCE: 018781-003910US
      ; CURRENT APPLICATION NUMBER: US/09/759,595
      ; CURRENT FILING DATE: 2001-01-13
      ; PRIOR FILING DATE: 2000-01-13
      ; NUMBER OF SEQ ID NOS: 7
      ; SOFTWARE: PatentIn Ver. 2.1
      ; SEQ ID NO 4
      ; LENGTH: 1542
      ; TYPE: DNA
      ; ORGANISM: Mus sp.
      ; FEATURE:
      ; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
      ; NAME/KEY: CDS
      ; LOCATION: (163)..(1542)
      ; OTHER INFORMATION: murine IRAK-4
      ; US-09-759-595-4

Alignment Scores:
Pred. No.:      7.87e-64      Length:      1542
Score:          476.00      Matches:      89
Percent Similarity: 95.92%      Conservative: 5
Best Local Similarity: 90.82%      Mismatches: 4
Query Match:    92.07%      Indels:      0
DB:             10      Gaps:      0

US-10-001-254-6 (1-98) x US-09-759-595-4 (1-1542)
Qy      1 ThTyrValArgCybLeuAsnValGlyLeuIleArgLyLeuSerAspPheIleaspPro 20
      187 ACATACATACGCAACCTTAATGTGGGATCCTTAGAGAGCTGTGGATTATTATGATCCT 246
      21 GlnGluGlyTTPlybLyLeuAlaValAlaIleLybSProSerGlyAspAspArgTyr 40
      247 CAAGAGGGGTGAGAGAAATTAGCAGTAGCTATCAAAAAGCCGTCGGCGACGACAGATAC 306
      41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlybSerProThrSer 60
      307 AATCAGTTCATATTAAGAGATTGCAACCTTACTTCAGACCGGAGAGAGCCCACTCTGT 366
      61 GluLeuLeuPheAspTTPGlyThrThraSncCybThrValGlyAspLeuValAspLeuLeu 80
      367 GAACCTGCTGTTGACTGGGGGACCAAGACTGACAGAGTGGCGACCTTGTGATCTACTG 426
      81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
      427 GTCCAGATTGAGCTGTTGGCCCGGCACCTCTCCGTGGCGGAGATGCCGTTCCC 480

RESULT 10
US-09-833-790-149
; Sequence 149, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Radooh
; APPLICANT: Indrias, Carol Y.
; APPLICANT: Fan, Liqun

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      ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
      ; FILE REFERENCE: 210121.512
      ; CURRENT APPLICATION NUMBER: US/09/833,790
      ; CURRENT FILING DATE: 2001-04-11
      ; NUMBER OF SEQ ID NOS: 440
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 149
      ; LENGTH: 501
      ; TYPE: DNA
      ; ORGANISM: Homo sapien
      ; FEATURE:
      ; NAME/KEY: misc feature
      ; LOCATION: (1) - (501)
      ; OTHER INFORMATION: n = A,T,C or G
      ; US-09-833-790-149

Alignment Scores:
Pred. No.:      1.21e-54      Length:      501
Score:          413.00      Matches:      93
Percent Similarity: 94.00%      Conservative: 1
Best Local Similarity: 93.00%      Mismatches: 4
Query Match:    79.88%      Indels:      4
DB:             9      Gaps:      0

US-10-001-254-6 (1-98) x US-09-833-790-149 (1-501)
Qy      1 ThTyrValArgCybLeuAsnValGlyLeuIleArgLyLeuSerAspPheIleaspPro 20
      45 ACATATGTGGCGCTGCCCAATGTGGACTAATTAGGAAGCTGTCAGATTATATGATCCT 104
      21 GlnGluGlyTTPlybLyLeuAlaValAlaIleLybSProSerGlyAspAspArgTyr 40
      105 CAGAGAGATGGAGAGAGATTAGCTGTGCTATTAAAGACATTTGATGATGATAC 164
      41 AsnGln-PheHisIleArgArgPheGluAlaLeuLeuGlnThrGlybSerProThrSe 60
      165 AATCAAGTTTCACATAGAGATTGGAAGCTT-CTTCAAACTGGAAGAAAGTCCACTTC 223
      60 rGluLeuLeuPheAspTTP-GlyThrThraSncCybThrValGlyAspLeuValAspLeu 80
      224 TTGAATCTGTTTGACCTGGGGGCGCCAAATTGACAGATGGATCTGTGATCTTT 283
      80 eulIleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
      284 TGATCCAAATGAATT-TTGTCTCTCGAGCTTTTGTCCAGATGCTGTTCC 338

RESULT 11
US-09-966-451-10
; Sequence 10, Application US/09966451
; Publication No. US20030087856A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-966-451-10

Alignment Scores:
Pred. No.:      1.95e-27      Length:      31000
Score:          256.00      Matches:      49
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 98.00%      Mismatches: 0
Query Match:    49.52%      Indels:      0
DB:             10      Gaps:      0

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US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)

QY 45 ILeArGArGpHeGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe 64
 Db 12963 TTAAGGAGATTGAGCATTTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTT 13022
 QY 65 AsPTpGlyThrThrAsnCyseThryValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
 Db 13023 GACTGGGGCACCACAAATTGCACAGTTGGTGAATCTTGTGATCTTTGATCCAAATGAA 13082
 QY 85 PhePheAlaProAlaSerLeuLeuPro 94
 Db 13083 TTTTTCCTCCTCGAGTCTTTTCCTCCA 13112

RESULT 12

US-10-630-399-10
 ; Sequence 10, Application US/10630399
 ; Publication No. US20040019009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freiler
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
 ; FILE REFERENCE: RTS-0324
 ; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US/09/966,451
 ; PRIOR FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 88
 ; SEQ ID NO 10
 ; LENGTH: 31000
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 US-10-630-399-10

Alignment Scores:
 Pred. No.: 1,956-27 Length: 31000
 Score: 256.00 Matches: 49
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.00% Mismatches: 0
 Query Match: 49.52% Indels: 0
 DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-630-399-10 (1-31000)

QY 45 ILeArGArGpHeGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe 64
 Db 12963 TTAAGGAGATTGAGCATTTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTT 13022
 QY 65 AsPTpGlyThrThrAsnCyseThryValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
 Db 13023 GACTGGGGCACCACAAATTGCACAGTTGGTGAATCTTGTGATCTTTGATCCAAATGAA 13082
 QY 85 PhePheAlaProAlaSerLeuLeuPro 94
 Db 13083 TTTTTCCTCCTCGAGTCTTTTCCTCCA 13112

RESULT 13

US-10-001-254-25
 ; Sequence 25, Application US/10001254
 ; Publication No. US20030049702A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Godzik, Adam
 ; APPLICANT: Pawlowski, Krzysztof
 ; APPLICANT: Fiorentino, Loredana
 ; APPLICANT: Lee, Sug Hyung
 ; APPLICANT: Roth, Wilfred
 ; APPLICANT: Steiner-Liwen, Frank
 ; TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins
 ; FILE REFERENCE: P-1J 5037
 ; CURRENT APPLICATION NUMBER: US/10/001,254

;; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/301,889
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 09/715,893
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25
 ; LENGTH: 211
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) ... (177)
 US-10-001-254-25

Alignment Scores:
 Pred. No.: 3,956-29 Length: 211
 Score: 247.00 Matches: 46
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.78% Indels: 0
 DB: 14 Gaps: 0

US-10-001-254-6 (1-98) x US-10-001-254-25 (1-211)

QY 1 ThrTyValaGyCyseLeuAsnValGlyLeuIleArGlyLysSerAspPheIleAspPro 20
 Db 25 ACATATGCGCGTGGCTCAATGTTGAGCTTAATGGAACTGTCAGATTATTTATGATCCT 84
 QY 21 GlnGlnGlyTrpTyValaLeuAlaValAlaIleLysProSerGlyAspAspAspGlyr 40
 Db 85 CAAGAAGATGGAAAGATTAGCTGTAGCTTTTAAAAAACCATGTGTGATGATAGATAC 144
 QY 41 AenGlnPheHisIleArg 46
 Db 145 AATCAGTTTCACATAGA 162

RESULT 14

US-10-242-535A-26096
 ; Sequence 26096, Application US/10242535A
 ; Publication No. US2004001363A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 26096
 ; LENGTH: 470
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-26096

Alignment Scores:
 Pred. No.: 1,256-28 Length: 470
 Score: 247.00 Matches: 46
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.78% Indels: 0
 DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-242-535A-26096 (1-470)

QY 1 ThrtYrValaIaGyCylsleuAsnVaIGlyleuIleArglylsleuSerAspPheIleAspPro 20
 DB 139 ACATATGTGCGCTCCCTCAATGTTGAGTAAGAGCTGTCAATTTATTGATCCT 198
 QY 21 GlnGluGlyTTPlylsYsleuAlaValAlaIlelylsYsProSerGlyAspAspArgTyr 40
 DB 199 CAAGAAGATGGAAGAGTTCCTGCTGCTATTAACCACTGCTGATGATGATAC 258
 QY 41 AsnGlnPheHisIleArg 46
 DB 259 AATCAGTTTCACATAGAG 276

RESULT 15

US-10-085-783A-26096
 ; Sequence 26096, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2002

; CURRENT APPLICATION NUMBER: US/10/085,783A

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 26096

; LENGTH: 470

; TYPE: DNA

; ORGANISM: Human

US-10-085-783A-26096

Alignment Scores:

Pred. No.: 1.25e-28 Length: 470
 Score: 247.00 Matches: 46
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.78% Indels: 0
 DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-085-783A-26096 (1-470)

QY 1 ThrtYrValaIaGyCylsleuAsnVaIGlyleuIleArglylsleuSerAspPheIleAspPro 20
 DB 139 ACATATGTGCGCTCCCTCAATGTTGAGTAAGAGCTGTCAATTTATTGATCCT 198
 QY 21 GlnGluGlyTTPlylsYsleuAlaValAlaIlelylsYsProSerGlyAspAspArgTyr 40
 DB 199 CAAGAAGATGGAAGAGTTCCTGCTGCTATTAACCACTGCTGATGATGATAC 258
 QY 41 AsnGlnPheHisIleArg 46
 DB 259 AATCAGTTTCACATAGAG 276

Search completed: January 12, 2005, 09:54:48
 Job time : 478 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 05:39:30 ; Search time 412 Seconds
(without alignments)
1248.649 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 413486 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	517	100.0	294	AAD59056 Human IRA
3	517	100.0	833	AA009319 Human can
4	517	100.0	1383	AAD40079 Human IRA
5	517	100.0	1383	AAD59061 Human IRA
6	517	100.0	1668	AA576805 DNA encod

7	517	100.0	2817	6	AAD40085	Aad40085 Human IRA
8	517	100.0	2817	6	AAD59067	Aad59067 Human IRA
9	517	100.0	2817	10	ACC47548	Acc47548 Human IL-
10	513	99.2	1383	5	AAD10197	Aad10197 Human int
11	476	92.1	1542	5	AAD10198	Aad10198 Mouse int
12	413	79.9	501	6	AA561608	Aa561608 Lung email
13	256	49.5	405	5	AA576803	AA576803 DNA encod
14	256	49.5	31000	10	ACC47549	Acc47549 Human DNA
15	247	47.8	211	6	AAD40084	Aad40084 Human IRA
16	247	47.8	211	6	AAD59066	Aad59066 Human IRA
17	247	47.8	415	5	AA576802	AA576802 DNA encod
18	247	47.8	2213	3	AAH13798	Aah13798 Human CDN
19	247	47.8	2432	12	ADB28369	Ab28369 Human KXP
20	134.5	26.0	408	6	ABO56733	Ab56733 Human col
21	96.5	18.7	1791	4	AAF44695	Aaf44695 Novel pro
22	96.5	18.7	1791	12	AD129393	Ad129393 Human MAR
23	96.5	18.7	2277	4	AA044459	Aa044459 Interleuk
24	96.5	18.7	2288	3	AAZ61602	Aaz61602 DNA encod
25	96.5	18.7	2293	4	AA157800	Aa157800 Human pol
26	96.5	18.7	2490	5	AA586902	Aa586902 DNA encod
27	95	18.4	1888	9	ADB61345	Adb61345 CDNA encod
28	84	16.2	1494	5	AA567194	Aa567194 DNA encod
29	79	15.3	1782	10	ADB40440	Adb40440 Human IRA
30	79	15.3	1806	2	AA577599	Aa577599 Human IRA
31	79	15.3	3459	2	AA577600	Aa577600 Human IRA
32	78.5	15.2	861	4	AA137224	Aa137224 Human mus
33	78.5	15.2	861	8	ABX60212	Abx60212 CDNA encod
34	78.5	15.2	861	12	ADJ30962	Adj30962 Human mus
35	78.5	15.2	864	4	AA137222	Aa137222 Human mus
36	78.5	15.2	864	4	AA137225	Aa137225 Human mus
37	78.5	15.2	864	8	ABX60213	Abx60213 CDNA encod
38	78.5	15.2	864	8	ABX60210	Abx60210 CDNA encod
39	78.5	15.2	864	12	ADJ30963	Adj30963 Human mus
40	78.5	15.2	864	12	ADJ30960	Adj30960 Human mus
41	77	14.9	756	9	AA57286	Aa57286 Murine My
42	75.5	14.6	3128	11	ADM02024	Adm02024 Human eos
43	74.5	14.4	652	6	ABK53369	Abk53369 Human eos
44	74.5	14.4	774	6	ABK73720	Abk73720 Bacillus
45	72.5	14.0	2819	6	ABK52386	Abk52386 DNA encod

ALIGNMENTS

RESULT 1	
AAD40074	standard; CDNA; 294 BP.
AC	AAD40074;
XX	
DT	22-OCT-2002 (first entry)
XX	
DS	Human IRAK4 DD (death domain) cDNA.
XX	
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW	NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW	inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW	immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW	Immunosuppressive; gene therapy; anticense therapy; gene; ss.
OS	Homo sapiens.
XX	
PH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..294
FT	/*tag= a
FT	/product= "Human IRAK4 DD"
FT	/note= "No start and stop codon"
XX	/partial
XX	
PN	W0200240680-A2.
XX	
PD	23-MAY-2002.
XX	
PF	15-NOV-2001; 2001WO-US044844.

XX 17-NOV-2000; 2000US-00715893.
PR 29-JUN-2001; 2001US-0301889P.
XX

PA (BURN-) BURHAM INST.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX

DR WPI; 2002-500222/53.
DR P-PSDB; AAE24854.

PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 18; Page 173-174; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. paltacti or a nucleic acid encoding the
CC CTDD DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 DD cDNA
XX

SO Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,666-64 Length: 294
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x AAD40074 (1-294)

QY 1 ThtTrrValaAGCGleuAsnValGlyLeuileAGlyLeuSerAspPheileAspPro 20
Db 1 ACAATATGCGCGCTCAATGTTGACTTAATAGGAAGCTGTCAGATTATGATCTCT 60
QY 21 GInGluGlyTTPLySLyLeuAlaValAlaIleLySLySPROSeGlyAspAspArgTy 40
Db 61 CAAGAAGATGGAAGAACTTACCTTACTTATTAAGAAACCACTCGGAGATGATGATAC 120
QY 41 AAGGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnInrGlyLySerProThrSer 60
Db 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAACTGAGAAAAGCCCACTTCT 180
QY 61 GluLeuLeuPheAspPTrGlyThThrasnGlySerThrValGlyAspLeuValAspLeu 80
Db 181 GAATTACTGTTTGACTGGGGGCAACCAAAATGACAGTTGGTGTGATCTTGTGATCTTTTG 240

QY 81 IIEGlnAsrGlnPhePheAlaProAlaSerleuLeuPProAspAlaValPro 98
Db 241 ATCCAAAAGAAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCC 294

RESULT 2

AAD59056
ID AAD59056 standard; cDNA; 294 BP.

XX AAD59056;

DT 18-DEC-2003 (first entry)

DE Human IRAK4 DD cDNA.

KW Human, death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neural growth factor receptor-interacting death domain; cell adhesion;
KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers
FT CDS 1..294
FT /tag= a
FT /product= "Human IRAK4 DD protein"
FT /note= "No start and stop codon"
FT /partial

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX

DR WPI; 2002-500222/53.
DR P-PSDB; AAE38897.

PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 18; Page 33-34; 99pp; English.

CC The present invention provides novel death domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,

CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching, DDE, DDEs and NB-ARC
 CC domains and/or anti-DD, anti-DDE or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 DD cDNA

XX SQ Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,66e-64	Length:	294
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-001-254-6 (1-98) x AAD59056 (1-294)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgIysLeuSerAppheilleaspPro 20
 DB 1 ACATATGTGGCGCTCCCAATGTTGACATAATTAGAGAGCTGTAGATTATGATCT 60
 QY 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleYlsYsProSerGlyAspAspArgTyr 40
 DB 61 CAGAGAGATGAGAGAGATTAGCTGTAGCTATTAAAAACCATCTGTGTAGATAGATAC 120
 QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyYsSerProThrSer 60
 DB 121 AATCAGTTTCACATTAAGAGATTGAAGCACTTACTCAAACTGGAAAAAGTCCCACTTCT 180
 QY 61 GluLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeu 80
 DB 181 GAATTACTGTTTGACTGGGGCACCAAAATTGCACAGTTGTGTGATCTTTG 240
 QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 DB 241 ATCCAAATGAATTTTGTCTCCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294

RESULT 3
 AAA09319 standard; DNA; 833 BP.

AC AAA09319;

DT 10-AUG-2000 (first entry)

XX Human cancer associated antigen precursor DNA, clone NY-REN-64.

XX Human cancer associated antigen precursor; diagnosis; cytostatic;

KM renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;

XX Homo sapiens.

OS Homo sapiens.

XX Key CDS Location/Qualifiers

XX Key CDS 50..670

XX Key CDS 50..670

XX Key CDS 50..670

XX Key CDS 50..670

PA (LUDW-) LUDWIG INST CANCER RES.

XX Obata Y, Gout I, Tureci O, Sahin U, Pfeundschn M, Scanlan MJ;

PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;

XX WPI; 2000-303774/26.

DR P-PSDB; AAY92347.

XX Preventing, diagnosing and/or treating disorders associated with abnormal

PT expression of human cancer associated antigens.

XX Claim 57; Page 85; 121pp; English.

XX AAA09310-20 are novel genes isolated by SEREX screening from a renal

CC cancer cell line 1973/10.4. The genes encode cancer associated antigen

CC precursors. These gene products are useful in methods for preventing,

CC diagnosing and/or treating disorders, especially cancer, associated with

CC abnormal expression of human cancer associated antigens. The method

CC comprises contacting a sample from a subject with an agent that

CC specifically binds to the nucleic acid molecule or expression product (or

CC fragment) complexed with a human leukocyte antigen (HLA) molecule and

CC determining the interaction between the agent and the nucleic acid

CC molecule or the expression product as a determination of the disorder

XX SQ Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14e-63	Length:	833
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-001-254-6 (1-98) x AAA09319 (1-833)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgIysLeuSerAppheilleaspPro 20
 DB 74 ACATATGTGGCGCTCCCAATGTTGACATAATTAGAGAGCTGTAGATTATGATCT 133
 QY 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleYlsYsProSerGlyAspAspArgTyr 40
 DB 134 CAGAGAGATGAGAGATTAGCTGTAGCTATTAAAAACCATCTGTGTAGATAGATAC 193
 QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyYsSerProThrSer 60
 DB 194 AATCAGTTTCACATTAAGAGATTGAAGCACTTACTCAAACTGGAAAAAGTCCCACTTCT 253
 QY 61 GluLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeu 80
 DB 254 GAATTACTGTTTGACTGGGGCACCAAAATTGCACAGTTGTGTGATCTTTG 313
 QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 DB 314 ATCCAAATGAATTTTGTCTCCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 4

AA040079

ID AAD40079 standard; DNA; 1383 BP.

AC AAD40079;

DT 22-OCT-2002 (first entry)

XX Human IRAK4 gene #1.

XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;

KM NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;

KM inflammation; allergy; autoimmunity; allograft rejection; cell division;

KM immune-based pathology; fibrosis; arthritis; graft versus host disease;

XX immunosuppressive; gene therapy; antisense therapy; gene; ds.

XX Homo sapiens.

```

XX Key Location/Qualifiers
FH CDS 1..1383
FT /tag= a
FT /product= "Human IRAK4"
PN WO200240680-A2.
XX
XX 23-MAY-2002.
XX
XX 15-NOV-2001; 2001MO-US044844.
XX
XX 17-NOV-2000; 2000US-00715893.
XX
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (BURN-) BURHAM INST.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Stenmer-Liwen F;
XX WPI; 2002-500222/53.
XX
XX P-PSDB; AAE24859.
XX
XX New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19, Page 180-182; 209pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a death
XX domain (DD), death effector domain (DED) or NB-ARC domain. The invention
XX is useful for identifying a binding agent, preferably a protein or a drug
XX that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
XX domain from DP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
XX NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
XX detecting the association of the domain and the candidate binding agent,
XX by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
XX chemical crosslinking, nuclear magnetic resonance (NMR), mass
XX spectroscopy (MS) and FPA. The invention is useful for modulating the
XX level of a cell process such as cell proliferation, cell adhesion, cell
XX stress responses, responses to microbial infection and B cell
XX immunoglobulin class switching, in particular apoptosis within a cell.
XX Antibody specifically reactive with CTDD DD of C. trachomatis, C.
XX muridarum, C. pneumoniae, and C. piteacti or a nucleic acid encoding the
XX CTDD DD protein is useful for detecting a Chlamydia infection. The
XX invention is useful for modulating the activity of oncogenic proteins,
XX for treating a pathology caused by the oncogenic proteins and for
XX treating bacterial infections by modulating the activity of bacterial
XX proteins. The protein and antibody specific for it are useful for
XX discovery of drugs that suppress infection, inflammation, allergy,
XX sepsis, autoimmunity, allograft rejection and other diseases. The protein
XX is useful for treating immune-based pathologies, pathologies associated
XX with cell division, inflammatory diseases such as sepsis, fibrosis,
XX arthritis, graft versus host disease. The invention is used in antisense
XX therapy and gene therapy. The present sequence is human IRAK4 gene
XX
XX Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No: 2,31e-63 Length: 1383
XX Score: 517.00 Matches: 98
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-10-001-254-6 (1-98) x AAD40079 (1-1383)
XX
XX 1 ThrlrValargCyVleuAsnValGlyLeuLeaIleuSerAspPheIleAspPro 20
XX |||||
XX 25 ACAATATGCGCTGCTCAATGTTGACTAATTAGAGAGCTGTCAGATTATTCATCCT 84
XX |||||
XX 21 GlnGlnGlyTlPlySLyLeuAlaValAlaIleSLySLyProSerGlyAspAspArgTyr 40
XX |||||

```

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DB 85 CAGGAAGATGAGAGAGAGTACCTAGCTATTAAAAACATCTGGGATAGATAC 144
XX |||||
QY 41 AenGlnPheHisIleArgArgPheGlnIleuLeuGlnInrGlySLySerProThrSer 60
XX |||||
DB 145 AATCAGTTTCACATTAAGAGATTTTGAAGCATTTACTTCAACTGGAAAAAGTCCACTTCT 204
XX |||||
QY 61 GlnLeuLeuPheAspTlPlyThrThraGlyValGlyAspLeuValAspLeuLeu 80
XX |||||
DB 205 GAATTAAGTCTGTTGACTGGGGGACACAAATTCACAGTTGGTGAATCTTGATCTTTTG 264
XX |||||
QY 81 IlleGlnAsnGlnPhePheAlaProIleSerLeuLeuLeuProAlaValAspPro 98
XX |||||
DB 265 ATCCAAATGAATTTTGTCTCTGCGAGCTCTTTGCTCCAGATGCTGTTCCTCC 318
XX |||||
XX
XX RESULT 5
XX AAD59061
XX ID AAD59061 standard; cDNA, 1383 BP.
XX
XX AAD59061;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human IRAK4 full length gene #1.
XX
XX Human; death Domain; DD; death effector domain; DED; cell proliferation;
XX Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
XX neural growth factor receptor-interacting death domain; cell adhesion;
XX vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
XX cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
XX apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
XX neoplasia; restenosis; immunosuppressive; antibody therapy; cytotoxic;
XX keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..1383
XX FT /tag= a
XX FT /product= "Human IRAK4 protein"
XX
XX US2003049702-A1.
XX
XX 13-MAR-2003.
XX
XX 15-NOV-2001; 2001US-00001254.
XX
XX 17-NOV-2000; 2000US-00715893.
XX
XX 17-NOV-2000; 2000US-0367360P.
XX
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (REED/) REED J C.
XX (GODZIK/) GODZIK A.
XX (PAWL/) PAWLOWSKI K.
XX (FIOR/) FIORENTINO L.
XX (LEES/) LEE S H.
XX (ROTH/) ROTH W.
XX (STEN/) STENNER-LIEWEN F.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Stenmer-Liwen F;
XX WPI; 2002-500222/53.
XX
XX P-PSDB; AAE38902.
XX
XX New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19, Fig 10A; 99pp; English.
XX
XX The present invention provides novel death Domain (DD) and death effector
XX domain (DED) proteins and nucleic acids encoding them. The invention also

```

CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTPD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DDEs and NB-ARC
CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC Interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
XX

Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,31e-63	Length:	1383
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-10-001-254-6 (1-98) x AAD59061 (1-1383)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspPheIleAaspPro 20
DB 25 ACATATGTGGCGCTCCCTCAATGTGGACTAATTTGGAAGCTGTGAGATTATTATGATCCT 84
QY 21 GlnGlnGlyTTPyLysLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGTYr 40
DB 85 CAAGAAAGATGAAGAAGATTAGCTGTAGCTATTAATAAACATCTGGATGATAGATAC 144
QY 41 AasnGlnPheHsIleArgArgPheGlnAlaLeuLeuGlnInrGlyLysSerProThSer 60
DB 145 AATCAGTTTCACTAAGAGATTGGAAGCATTTCTTCAAACTGAAAAAGTCCCATCTCT 204
QY 61 GluLeuLeuPheAepTPGlyThrThrAasnCysThrValGlyAaspLeuValAaspLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGTGATCTTGGATCTTTTG 264
QY 81 IleGlnAasnGlnPhePheAlaProAlaSerLeuLeuLeuProAapAlaValPro 98
DB 265 ATCCAAATGAAATTTTGTCTCGCAGTCTTTTGTCTCCCAAGTGTCTTCCC 318

RESULT 6

AAS76805 standard; cDNA; 1668 BP.

XX AAS76805;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #12609.

XX Human chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US006631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR P-PSDB; ABG32618.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 12609; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,39e-63	Length:	1668
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-10-001-254-6 (1-98) x AAS76805 (1-1668)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspPheIleAaspPro 20
DB 25 ACATATGTGGCGCTCCCTCAATGTGGACTAATTTGGAAGCTGTGAGATTATTATGATCCT 84
QY 21 GlnGlnGlyTTPyLysLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGTYr 40
DB 85 CAAGAAAGATGAAGAAGATTAGCTGTAGCTATTAATAAACATCTGGATGATAGATAC 144
QY 41 AasnGlnPheHsIleArgArgPheGlnAlaLeuLeuGlnInrGlyLysSerProThSer 60
DB 145 AATCAGTTTCACTAAGAGATTGGAAGCATTTCTTCAAACTGAAAAAGTCCCATCTCT 204
QY 61 GluLeuLeuPheAepTPGlyThrThrAasnCysThrValGlyAaspLeuValAaspLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGTGATCTTGGATCTTTTG 264
QY 81 IleGlnAasnGlnPhePheAlaProAlaSerLeuLeuLeuProAapAlaValPro 98
DB 265 ATCCAAATGAAATTTTGTCTCGCAGTCTTTTGTCTCCCAAGTGTCTTCCC 318

RESULT 7
 AAD40085 standard; DNA; 2817 BP.
 AAD40085;
 22-OCT-2002 (first entry)
 Human IRAK4 gene #2.
 Human IRAK4 gene #2.
 Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 50..1432
 /*tag= a
 /product= "Human IRAK4"
 WO200240680-A2.
 23-MAY-2002.
 15-NOV-2001; 2001MO-US044844.
 17-NOV-2000; 2000US-00715893.
 29-JUN-2001; 2001US-0301889P.
 (BURN-) BURNHAM INST.
 Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W, Stemmer-Liwen F,
 P-PSDB; AAE2465.
 WPI; 2002-500222/53.
 P-PSDB; AAE2465.
 New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 Claim 19; Page 194-196; 209pp; English.
 The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTMD (Chlamydia trachomatis DD protein), DED4 or NID (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and PPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTMD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTMD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 gene

SO Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,22e-63 Length: 2817
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-10-001-254-6 (1-98) x AAD40085 (1-2817)
 QY 1 ThrTyrValArgCysLeuAsnValGlyLeuArgLysLeuSerAspPheIleAspPro 20
 Db 74 ACATATGTCGCTGCTCAATGTGTGACTAATGGAAGCTGTCAATTTATTTGATCTT 133
 QY 21 GINGLUGLYTTPYLALYSLEUALAVALAIALELYSLYSPROSERGLYASAPASPTYR 40
 Db 134 CAAGAAGATGGAAGAAGTTAGCTGTACTTTAAAAACCATCTGTGATGATAC 193
 QY 41 AAGGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
 Db 194 AATCAGTTTCACATTAAGAGATTGAGACATTACTTCAAACTGGAAGAACTCCACTTCT 253
 QY 61 GIULEULEPHEAPSTTPGTYThr-ThrAsnCysThrValGlyAspLeuValAspLeuLan 80
 Db 254 GAATTACGTGTTGACTGGGCAACACAAATTGCAAGATGGATGATCTTGATGATCTTGG 313
 QY 81 ILEGIANGLUPHEPHEALAPROALASERLEULEUENLEUPROAPALVALPRO 98
 Db 314 ATCCAAAATGAATTTTTTGTCTCGCAGTCTTTTGTCTCCCAAGTGTCTTCC 367
 RESULT 8
 AAD59067 standard; CDNA; 2817 BP.
 AAD59067;
 18-DEC-2003 (first entry)
 Human IRAK4 full length gene #2.
 Human; death domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTMD; cell stress response; benign prostatic hypertrophy; antibacterial; NID; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 1..1432
 /*tag= a
 /product= "Human IRAK4 protein"
 US2003049702-A1.
 13-MAR-2003.
 15-NOV-2001; 2001US-00001254.
 17-NOV-2000; 2000US-00715893.
 17-NOV-2000; 2000US-0367360P.
 29-JUN-2001; 2001US-0301889P.
 (REED/) REED J C.
 (GODZ/) GODZIK A.
 (PAWL/) PAWLOWSKI K.
 (FIOR/) FIORENTINO L.
 (LEES/) LEE S H.

PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Stenner-Liewen F;
XX
DR WPI: 2002-500222/53.
DR P-PSDB: AAE38908.
XX
XX New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 18; Page 51-53; 99pp; English.
XX
XX The present invention provides novel death Domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neural growth factor
CC receptor-interacting protein (CTDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDB with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DEDs, DEDs and NB-ARC
CC domains and/or anti-DD, anti-DD or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
XX
SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,22e-63 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-001-254-6 (1-98) x AAD59067 (1-2817)

QY 1 ThrTyrValArgCySLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
Db 74 ACATATGTGGCGCTCCTCAATGTTGACTAATTAAGAAAGCTGACGATTTATGATCCT 133
QY 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysIleProSerGlyAspAspArgTyr 40
Db 134 CAAGAAGGATGAAAGATGAGTGTGATTAATAAACAATCTGGTGATGATGATAC 193
QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACATRAGAGATTTGAGCATTAATCTCAATGAGAAAGCCCACTTCT 253
QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCySThrValGlyAspLeuValAspLeu 80
Db 254 GAATTACTGTTTGACTGGGACCAACAATTGACAGTTGGTGTGATCTTGATCTTTTG 313
QY 81 IlleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAlaValPro 98
Db 314 ATCCAAATGATTTTGTCTCTGCGAGCTCTTGTCTCCACGATGCTGTCC 367
RESULT 9
ACCA7548

ID ACC47548 standard; DNA; 2817 BP.
XX
AC ACC47548;
XX
DT 11-JUL-2003 (first entry)
XX
DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.
XX
XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
KM interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
KM inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
XX gene; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..1432
FT /*tag=a
FT /product="IL-1 receptor-associated kinase-4"
XX
XX MO2003028636-A2.
XX
XX 10-APR-2003.
XX
XX 26-SEP-2002; 2002MO-US030574.
XX
XX 28-SEP-2001; 2001US-00966451.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Freiler SM;
XX
XX WPI: 2003-363256/34.
XX
XX P-PSDB; ABR44401.
XX
XX New antisense oligonucleotides for modulating IL-1 receptor-associated
PT kinase-4 gene expression, particularly useful for preventing, delaying or
PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
PT infection.
XX
XX
XX Example 13; Page 80-83; 119pp; English.
XX
XX The invention relates to a compound of 8-50 nucleobases which is targeted
CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
CC the expression of the encoded product. Also disclosed is the compound
CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
CC oligonucleotide is useful for treating an animal having a disease or
CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
CC (particularly renal cancer), inflammatory disease or an infection. The
CC antisense compounds are useful for diagnostics, therapeutics,
CC prophylaxis, or as research reagents or kits. The current sequence
CC represents the human IL-1 receptor-associated kinase-4 encoding sequence
CC (GenBank accession number NM_016123)
XX
SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,22e-63 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10
US-10-001-254-6 (1-98) x ACC47548 (1-2817)

QY 1 ThrTyrValArgCySLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
Db 74 ACATATGTGGCGCTCCTCAATGTTGACTAATTAAGAAAGCTGACGATTTATGATCCT 133
QY 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysIleProSerGlyAspAspArgTyr 40

Dd		134	CAGGAAGATGGAAGAAGTTTACGTCTTGACTATTAAAAACATCTGGTAGTAAGATAC	197
Oy		41	AerGlnPheHtSIleAgaGrpHeGluAlaLeuEugLInThrGIlySerProThrSer	60
Dd		194	AATCAAGTTTCACATAAGAGAAATTTGAAAGCATTTACTCTCAAATCGAAAAAGCCACATCTC	253
Oy		61	GluLeuLeuPheAspTrpGIlyThrThrAsnCysThrValGIlyAspLeuValAspLeuLeu	80
Dd		254	GAATTACTGTTTTAGCTGGGCCGCACACAATTGCACAGTTGGTAGTACTTTGGAGATCTTTTG	313
Oy		81	IleGlnAsnGlnPhePheAlaProAlaSerIleuLeuLeuProAspAlaValPro	98
Dd		314	ATCCAAAATGAATTTTGTCTCTCGTCGAGTCTTTTGCTCCAGATGCTGTTCCC	367
RESULT 10				
ID	AAD10197			
XX	AAD10197 standard; cDNA; 1383 BP.			
AC	AAD10197;			
DT	24-SEP-2001 (first entry)			
DE	Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.			
KM	Human, interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;			
KM	IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; CPD;			
KM	chronic obstructive pulmonary disease; neutropenictive; chronic cough;			
KM	adult respiratory disease syndrome; pulmonary fibrosis; ashma; ARDS;			
KM	interstitial lung disease; allergic rhinitis; transplant rejection;			
KM	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;			
KM	multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;			
KM	cardiovascular disease; atherosclerosis; neurodegenerative disease;			
KM	sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;			
KM	inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;			
KM	Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;			
KM	sarcoidosis; transgenic animal, ss.			
OS	Homo sapiens.			
FT	Key	Location/Qualifiers		
FT	CDS	1..1383		
FT		/tag= a		
FT		/product= "Human IRAK-4"		
XX				
PV	WO200151641-A1.			
PD	19-JUL-2001.			
PF	12-JAN-2001; 2001WO-US001171.			
PR	13-JAN-2000; 2000US-0176395P.			
PA	(TUDA-) TUDARIK INC.			
EA				
PI	Wesche H, Li S;			
DR	WPI; 2001-451860/48.			
DR	P-FSDB; AAB05398.			
XX				
PT	Novel human interleukin-1 receptor associated kinase polypeptide, useful			
PT	for identifying modulators of the polypeptide for treating gout, asthma,			
PT	allergic rhinitis, multiple sclerosis and skin cancer.			
XX				
PS	Claim 7, Fig 2; 89pp. English.			
CC	The present sequence is a cDNA encoding human interleukin (IL)-1 receptor			
CC	associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and			
CC	other receptors and act to transduce signals originating from the			
CC	activated receptors, ultimately leading to a variety of downstream			
CC	effects such as nuclear factor (NF)-kappaB activation. The IRAK-4			
CC	inhibitors are useful for treating inflammatory diseases such as			
CC	pulmonary diseases and diseases of the airway (e.g., adult respiratory			

CC	diseases syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
CC	pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
CC	allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
CC	rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
CC	diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
CC	cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
CC	the central nervous system (e.g., neurodegenerative disease), CD4
CC	mediated sepsis, non-CD4 mediated sepsis, osteoarthritis, osteoporosis,
CC	psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
CC	dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
CC	ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
CC	sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
CC	IRAK-4 activity or expression are used to inhibit signal transduction
CC	resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
CC	receptor in a cell. They also inhibit the activation of a transcription
CC	factor that activates NF-kappaB in the cell. IRAK-4 is used to create a
CC	nonhuman transgenic animal which is useful for testing the function of
CC	IRAK-4 in vivo, to generate models for the study of inflammatory
CC	disorders and conditions and for the development of potential treatments
CC	for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
CC	are also used in gene therapy and in antisense therapy
CC	XX
SQ	Sequence 1383 BP, 463 A, 244 C, 283 G, 393 T, 0 U, 0 Other,
Alignment Scores:	
Pred. No.:	8.59e-63 Length: 1383
Score:	513.00 Matches: 97
Percent Similarity:	98.98% Conservative: 0
Best Local Similarity:	98.98% Mismatches: 1
Query Match:	99.23% Gaps: 0
DB:	5
US-10-001-254-6 (1-98) x AAD10197 (1-1383)	
OY	1 ThrTyrValArgGcyVeluenuValGlyLeuIleArgGlySleuSerAepPheIleapPro 20
DB	25 ACATAGTGGCGCTGCCTCATATGTGACCTAAATAGGAAGCGTGCAGATTTATGAACTT 84
OY	21 GlnGlnGlyTyrPylSylSleuAlaValAlaIleTylSylProSerGlyAaspArgTyr 40
DB	85 CAAGAAGATGAGAAAGAAAGTTACTGTAGCTATTAAAAACATCTGGTGAATGATAGTAC 144
OY	41 AsnGlnPheHsIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysProThrSer 60
DB	145 AATCAGTTTCACATTAAGAGATTTAACCATTTACTCTCAATCGAATAAGGCCACATCTCT 204
OY	61 GluLeuLeuPheAepTyrPglYlThrThraSerCysThrTyrValGlyAspLeuAlaPheLeu 80
DB	205 GAATTACTGTTTGCATCGGGGACACCAAAATTCGACAGCTGTATCTTGTGGATCTTTTG 264
OY	81 IleGlnAsnGlnPhePheAlaProIleAserLeuLeuPheProApeAlaValPro 98
DB	265 ATCCAAAAGAAATTTTGTCTCTCGAGAGTCTTTTGTCTCCAGATGCTGTTCC 318
ID	AAD10198 standard, cDNA, 1542 BP.
XX	AAD10198
XX	24-SEP-2001 (first entry)
XX	Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
XX	Mouse, interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
XX	IL, antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
XX	chronic obstructive pulmonary disease; neuroprotective; chronic cough;
XX	adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
XX	interstitial lung disease; allergic rhinitis; transplant rejection;
XX	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX	multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
XX	cardiovascular disease; atherosclerosis; neurodegenerative disease;
XX	sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;

CC lung cancer in a patient. An isolated T cell population is useful for
 CC removing tumor cells from the biological sample and for inhibiting the
 CC development of cancer in a patient. AAS61460-AAS61874 represent novel
 CC human lung small cell cancer antigen coding sequences of the invention
 XX

Sequence 501 BP; 166 A; 102 C; 97 G; 134 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 4,01e-49 Length: 501
 Score: 413.00 Matches: 93
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 93.00% Mismatches: 4
 Query Match: 79.88% Indels: 4
 DB: 6 Gaps: 0
 US-10-001-254-6 (1-98) x AAS61608 (1-501)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAapPro 20
 Db 45 ACATATGTCGCGCTGCCTCAATGTGGACTAATAGGAAGCTGCAGATTTTATGATCCT 104
 QY 21 GlnGlnGlyTTPDlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspAlyTyr 40
 Db 105 CAAGAGGATGGAGAGAGATTAGCTGATTAATAAAACCAATCTGTGATGATAGATAC 164
 QY 41 AsnGln-PheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThise 60
 Db 165 AATCAAGTTTCACATAGAGAGATTGAGACATT-CTTCAAACTGGAAAAAGTCCCACTTC 223
 QY 60 rGlnLeuLeuPheAapTTP-GlyThrThrAsnCysThrValGlyAspLeuValAspLeuL 80
 Db 224 TTGAAATACGTGTGACTGGGCGGCACCAAAATTTGACAGTGTGTGATCTTGGATCTTT 283
 QY 80 euIleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAlaValAlPro 98
 Db 284 TGAATCCAAATGAAATT-TTGTCTCCGCGAGTCTTTTGTCTCCAGAGTGTTC 338
 RESULT 13
 AAS76803
 ID AAS76803 standard; CDNA; 405 BP.
 XX
 AC AAS76803;
 XX
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #12607.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 XX
 DR P-PSDB; ABG12616.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

PS Claim 1; SEQ ID NO 12607; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (II) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7.96e-27 Length: 405
 Score: 256.00 Matches: 49
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.00% Mismatches: 0
 Query Match: 49.52% Indels: 0
 DB: 5 Gaps: 0

US-10-001-254-6 (1-98) x AAS76803 (1-405)

QY 45 IleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSerGlyLeuLeuPhe 64
 Db 114 TTAGGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTGAATTAAGTTT 173
 QY 65 AapTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuIleGlnAsnGln 84
 Db 174 GACTGGGGGACCAAAATTTGACAGTGTGTGATCTTGTGATCTTGTGATCAAAATGAA 233
 QY 85 PhePheAlaProAlaSerLeuLeuPro 94
 Db 234 TTTTGTCTCTCGCAGTCTTTGTCTCCCA 263
 RESULT 14
 ACC47549
 ID ACC47549 standard; DNA; 31000 BP.
 XX
 AC ACC47549;
 XX
 DT 11-JUL-2003 (first entry)
 DE Human DNA complement sequence # SEQ ID 10.
 XX
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX

PA (ISIS-) ISIS PHARM INC.
XX Bennett FC, Freier SM;
PI WPI; 2003-363256/34.
XX
DR
XX
PT New antisense oligonucleotides for modulating IL-1 receptor-associated
PT kinase-4 gene expression, particularly useful for preventing, delaying or
PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
PT infection.
XX
PS Example 15; Page 85-102; 119pp; English.
XX
CC The invention relates to a compound of 8-50 nucleobases which is targeted
CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
CC the expression of the encoded product. Also disclosed is the compound
CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
CC oligonucleotide is useful for treating an animal having a disease or
CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
CC (particularly renal cancer), inflammatory disease or an infection. The
CC antisense compounds are useful for diagnostics, therapeutics,
CC prophylaxis, or as research reagents or kits. The current sequence is
CC utilized in an example from the invention in the design of antisense
CC oligonucleotides, and represents the complement of the human DNA sequence
CC that is given as Genbank accession number AC016143
XX
SQ Sequence 31000 BP; 9247 A; 5856 C; 5924 G; 9973 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.38e-24 Length: 31000
Score: 256.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
DB: 10 Gaps: 0
US-10-001-254-6 (1-98) x ACC47549 (1-31000)
QY 45 IleaRgArpPheGluAlaLeuLeuGlnThrGlySerProThrSerGlnLeuLeuPhe 64
Db 12963 TTAAGAGATTGAAGATTCTTCAAACTGAAAACTCCCACTTGATTTCTGTTT 13022
QY 65 AspTrpGlyThrThrAsnCyseThyValGlyAspLeuValAspLeuLeuGlnAsnGlu 84
Db 13023 GACTGGGCGCACCAAAATGCAAGTTGGTGTGATCTTTGATCCAAATGAA 13082
QY 85 PhePheAlaProAlaSerLeuLeuPro 94
Db 13083 TTTTGTCTCTGCGAGCTTTGTCTCCA 13112
RESULT 15
AAD40084
ID AAD40084 standard; DNA; 211 BP.
XX
AC AAD40084;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human IRAK4 short gene.
XX
KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW immunosuppressive; gene therapy; antisense therapy; gene; de.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..180
FT /*tag= a
FT

FT /product= "Human IRAK4 short protein"
XX
XX WO200240680-A2.
XX
XX 23-MAY-2002.
XX
XX 15-NOV-2001; 2001WO-US044844.
XX
XX 17-NOV-2000; 2000US-00715893.
XX
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Steiner-Liwen F;
PI WPI; 2002-500222/53.
DR P-PSDB; AAE24864.
XX
XX New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 19; Page 195; 209pp; English.
XX
CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDP (Chlamydia trachomatis DD protein), DED4 or
CC NIND (NGPR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDP DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDP DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 short gene
XX
SQ Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.19e-26 Length: 211
Score: 247.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.78% Indels: 0
DB: 6 Gaps: 0
US-10-001-254-6 (1-98) x AAD40084 (1-211)
QY 1 ThrTyValArgCyseLeuAsnValGlyLeuLeuArgYseuSerAaspPheLeaSPPro 20
Db 25 ACATATGTGGCGCTCCCTCAATGTTGCACTAATTAGGAAGCTGTGACTTTTATGATCCT 84
QY 21 GlnGlnGlyTTPlyVlyVlyLeuAlaValAlaLeuVlySPProSerGlyAspAspArgTyr 40
Db 85 CAAGAAGAGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGTGTGATGATGATAC 144
QY 41 AsnGlnPheHisLeuArg 46

Db |||||||
 145 AATCAGTTTCACATAAGA 162

Search completed: January 12, 2005, 07:14:08
Job time : 421 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 06:22:23 / Search time 2550 Seconds

(without alignments)
1400.429 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517

Sequence: 1 TYVCLNVGIRKLSDFIDP.....LTIQNEFPAPASLLPDAVP 98

Scoring table: BIOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool_h/US10001254/runat.10012005.172739.10471/app.query.fasta.1.263
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biobum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=400 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001254 @CGN 1.1 3437 @runat.10012005.172739.10471 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g981:*
9: gb_g982:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	517	100.0	859	4	BG164491 602342026
2	511	98.8	821	2	CK459029 923479 MA
3	509	98.5	811	4	BG616438 602642772
4	495	95.7	402	2	BR482619 168463 BA
5	495	95.7	666	7	CN788062 4122347 B
6	485	93.8	719	2	BR696981 602130160
7	476	92.1	598	5	CA538859 C0272B01-
8	476	92.1	598	5	BO552228 H4014C09-
9	476	92.1	610	2	BB660378 BB660378

10	476	92.1	637	2	BB613447
11	476	92.1	638	6	BY721552
12	476	92.1	663	6	BY726858
13	476	92.1	676	2	BB613167
14	476	92.1	1161	3	AK020397
15	476	92.1	2481	3	AK028837
16	476	92.1	2810	3	AK029028
17	476	92.1	575	5	BX522921
18	450	87.0	1383	9	AY418791
19	443	85.7	1383	9	AY418792
20	430.5	83.3	524	2	AM106160
21	415.5	80.4	1286	2	AY418793
22	415	80.3	541	4	BG691069
23	414.5	76.0	457	2	BB866698
24	393	76.0	503	2	BB8660349
25	393	76.0	852	5	BU209111
26	389	75.2	600	1	AJ453616
27	389	75.2	670	1	AJ447581
28	369	71.4	265	2	AM436511
29	359	69.4	686	7	CN066297
30	359	69.4	711	7	CN067840
31	359	69.4	775	7	CN061000
32	359	69.4	782	7	CN064552
33	349	67.5	313	4	BM151935
34	346	66.9	417	7	CO780006
35	343	66.3	606	1	AL647125
36	323.5	62.6	664	4	BU035962
37	319	61.7	479	7	CR370093
38	319	61.7	689	7	CR375297
39	319	61.7	793	5	EX876165
40	310	60.0	599	4	BU691338
41	296	57.3	632	6	CA365604
42	289	55.9	743	6	CA474136
43	289	55.9	815	7	CR866056
44	287	55.5	555	2	AM423082
45	287	55.5	771	7	CN507749

ALIGNMENTS

RESULT 1
BG164491 859 bp mRNA linear EST 06-FEB-2001
LOCUS 602342026F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4452055 5',
DEFINITION mRNA sequence.
ACCESSION BG164491.1 GI:12671194
VERSION BG164491.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://Image.lnl.gov
Plate: LLM10240 row: d column: 08
High quality sequence stop: 634.

FEATURES

1. 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4452055"

/tissue_type="hypenephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	7.9e-60	Length:	859
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-001-254-6 (1-98) x BG164491 (1-859)

OY 1 ThTtYValaTgCysLeuAenValGlyLeuIlleArgLysLeuSerAaspPheIlleAaspPro 20
DB 59 ACATATGTCGCGCTCCATGTTGACTTAATAGAAAGTTGTCAGATTTTATTGATCCT 118
OY 21 GINGUGLYTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGlyr 40
DB 119 CAAGAAAGATGGAAGAAGTTAGCTGATTAATAAACCATCTGGTGAATGATGATAC 178
OY 41 AaAGlnPheHsiIleArgArgPheGlnAlaLeuLenglnThrGlyLysSerProThrSer 60
DB 179 AATCAGTTTCATATAGAGATTTGAAAGATTTCACTCAAACTGAAAAAATCCACACTTC 238
OY 61 GluLeuLeuPheAspTTPGlyThrThrasnCySThrValGlyAaspLeuValAaspLeu 80
DB 239 GAATTAAGTCTTGTGCTGGGACACCAAAATTCGACAGTTGCTGATCTTGATCTTTG 298
OY 81 IleglnaAGlnPhePheAlaProAlaSerLeuLeuProAaspAlaValPro 98
DB 299 ATCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 352

RESULT 2
LOCUS CK459029 821 bp mRNA linear EST 14-JAN-2004
DEFINITION 923479 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CK459029
VERSION CK459029.1 GI:40830310
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS Smlth,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keeler,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
Plate: TMM8032 row: K column: 23
Seq primer: GTAAATGACATCATATGAGG.

FEATURES

source location/Qualifiers
1..821
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:

Pred. No.:	4.92e-59	Length:	821
Score:	511.00	Matches:	96
Percent Similarity:	98.98%	Conservative:	1
Best Local Similarity:	97.96%	Mismatches:	0
Query Match:	98.84%	Indels:	0
DB:	7	Gaps:	0

US-10-001-254-6 (1-98) x CK459029 (1-821)

OY 1 ThTtYValaTgCysLeuAenValGlyLeuIlleArgLysLeuSerAaspPheIlleAaspPro 20
DB 233 ACATATGTCGCGCTCCATGTTGACTTAATAGAAAGTTGTCAGATTTTATTGATCCT 292
OY 21 GINGUGLYTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGlyr 40
DB 293 CAAGAAAGATGGAAGAAGTTAGCTGATTAATAAACCATCTGGTGAATGATGATAC 352
OY 41 AaAGlnPheHsiIleArgArgPheGlnAlaLeuLenglnThrGlyLysSerProThrSer 60
DB 353 AACCAAGTTTCATATAGAGATTTGAAAGATTTCACTCAAACTGAAAAAATCCACACTTC 412
OY 61 GluLeuLeuPheAspTTPGlyThrThrasnCySThrValGlyAaspLeuValAaspLeu 80
DB 413 GAATTAAGTCTTGTGCTGGGACACCAAAATTCGACAGTTGCTGATCTTGATCTTTG 472
OY 81 IleglnaAGlnPhePheAlaProAlaSerLeuLeuProAaspAlaValPro 98
DB 473 GTCCAAATGAAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 526

RESULT 3
LOCUS BG616438 811 bp mRNA linear EST 18-APR-2001
DEFINITION 60264277291 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773760 5',
mRNA sequence.
ACCESSION BG616438
VERSION BG616438.1 GI:13667809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC

CNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1645 row: p column: 17
High quality sequence start: 3
High quality sequence stop: 613.
Location/Qualifiers

FEATURES

source location/Qualifiers
1..811
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4773760"
/tissue_type="embryonal carcinoma"

/lab_host="DH10B (T1 phage-resistant)"
/clone_1id="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccatcgcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:

Pred. No.:	9,09e-59	Length:	811
Score:	509.00	Matches:	97
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	1
Query Match:	98.45%	Indels:	0
DB:	4	Gaps:	0

US-10-001-254-6 (1-98) x BE616438 (1-811)

Qy 1 ThTtYrValaArgCySLuAuEnValGlyLeuIlleArySLuSerAaPheIlleAaSPPro 20
Db 77 ACATATGTCGCTCCCTCAATGTTGACTAATTAAGAGCTGTCAGATTATTAATGATCCT 136
Qy 21 GlnGluGlyTTPySLySLuAlaValAlaIleSLySPProSerGIyAaSPaSPaSTyr 40
Db 137 CAGAGAGATGAGAGAGATTAGCTGTAGCTATTAAGAACATCTCGTGAATGATGATAC 196
Qy 41 AaGlnPheHsIleAgaPheGluAlaLeuLeuGlnThrGlyLysSerProThSer 60
Db 197 AATCAGTTTCACATAGAGATTGAAGCATTTACTTCAATCGGAAAGTCCCACTTCT 256
Qy 61 GluLeuLeuPheAaPTTPGlyThrThraSncYerThrValGlyAaPLeuValaSPLeu 80
Db 257 GAATTACTGTTGACTGGGGCACCAAAATTCACAGTTGGTGAATCTTGGAATCTTTTG 316
Qy 81 IlleGlnAaGluPhePheAlaProAlaSerLeuLeuLeuProAaPAlaValPro 98
Db 317 ATCAAAATGATTTTCTGCTCCGCGAGCTTTTGTCCAGATGCTGTTCCC 370

RESULT 4 BE482619 402 bp mRNA linear EST 27-MAR-2003
LOCUS BE482619 168463 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE482619 GI:9602152
VERSION BE482619.1 GI:9602152
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1. (bases 1 to 402)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)

TITLE Contact: Sonstegard TS
JOURNAL USA, ARS, Beltsville Agricultural Research Center
MEDLINE Bldg. 200 Km 2A, Beltsville, MD 20705, USA
PUBMED Tel: 301 504 8416
12140684 Fax: 301 504 8414
COMMENT Email: tads@psl.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTACACAG
Plate: 11 row: F column: 7
Seq primer: ATTATGTCGACATATG.
Location/Qualifiers
1. 402

FEATURES

SOURCE

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1id="BARC_5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN

Alignment Scores:

Pred. No.:	2.89e-57	Length:	402
Score:	495.00	Matches:	92
Percent Similarity:	97.96%	Conservative:	4
Best Local Similarity:	93.88%	Mismatches:	2
Query Match:	95.74%	Indels:	0
DB:	2	Gaps:	0

US-10-001-254-6 (1-98) x BE482619 (1-402)

Qy 1 ThTtYrValaArgCySLuAuEnValGlyLeuIlleArySLuSerAaPheIlleAaSPPro 20
Db 88 ACATATGTCGCTCCCTCAATGTTGACTAATTAAGAGCTGTCAGATTATTAATGATCCT 147
Qy 21 GlnGluGlyTTPySLySLuAlaValAlaIleSLySPProSerGIyAaSPaSPaSTyr 40
Db 148 CAGAGAGATGAGAGATTAGAGCTGCTATTAAGAACATCTGGTGAATGATGATAC 207
Qy 41 AaGlnPheHsIleAgaPheGluAlaLeuLeuGlnThrGlyLysSerProThSer 60
Db 208 AATCAGTTTCACATAGAGATTGAAGCATTTACTCGAAATGGAAAGCCCACTGCT 267
Qy 61 GluLeuLeuPheAaPTTPGlyThrThraSncYerThrValGlyAaPLeuValaSPLeu 80
Db 268 GAGTTACTGTTGACTGGGGCACCAAAATTCACAGTTGGTGAATCTTGGAATCTTTTG 327
Qy 81 IlleGlnAaGluPhePheAlaProAlaSerLeuLeuLeuProAaPAlaValPro 98
Db 328 GTCAAAATGATTTTGTGCTCCGCGAGCTTTTGTCTACAGATGCTGTAACC 381

RESULT 5 CN788062 666 bp mRNA linear EST 26-MAY-2004
LOCUS CN788062 4122347 BARC 8BOV Bos taurus cDNA clone 8BOV_26007 5', mRNA
ACCESSION CN788062 GI:47684042
VERSION CN788062.1 GI:47684042
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1. (bases 1 to 666)
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
Matukumalli,L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
JOURNAL Contact: Richard G. Baumann
COMMENT Bovine Functional Genomics Lab

ANRI
BLUG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '-trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18
Plate: 26 row: 0 column: 07
Seq primer: CCTATTAGTGTGACACTATGAGAC
High quality sequence stop: 666.

FEATURES

source

Location/Qualifiers
1..666
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9113"
/clone="8BOV 26007"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_id="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, proximal duodenum,
jejunum, distal ileum, colon, 1/5 Neonatal, proximal
duodenum, jejunum, distal ileum"

ORIGIN

Alignment Scores:

Pred. No.: 5.74e-57 Length: 666
Score: 495.00 Matches: 92
Percent Similarity: 97.96% Conservative: 4
Best Local Similarity: 93.88% Mismatches: 2
Query Match: 95.74% Indels: 0
DB: 7 Gaps: 0

US-10-001-254-6 (1-98) x CN788062 (1-666)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspheIleApro 20
DB 69 ACATACGTGCGCGCTCCCTGCTGACTTAATTAAGAGTGTGCCATTTTATGATCCT 128
QY 21 GlnGluGlyTTPlySLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGlyr 40
DB 129 CAGAAGAGATGAGAAAGATTAGCAGTCGCTATTAACCAATCTGCTGATGATATAC 188
QY 41 AaenGlnPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrsr 60
DB 189 AATCAGTTTCACATTAAGAGATTGAAAGATTACTCAATTAAGAAAGCCCAAGTGT 248
QY 61 GluLeuLeuPheAaspTTPGlyThrThraenCysThrValGlyAaspLeuValAaspLeu 80
DB 249 GAGTTACTGTTTGCATCGGGCACCAAAATTGCACAGTTTGATTTTGTGATATTTTG 308
QY 81 IlegInaenGluPhePheAlaProAlaSerLeuLeuProAaspAlaValApro 98
DB 309 GTCCAAATGAGATTGCTTTCCTCCCTGCAAGTCTTTTGTCTACAGATGCTGTACCC 362

RESULT 6

BF696981

LOCUS 719 bp mRNA linear EST 22-DEC-2000
DEFINITION 602130160P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5',
mRNA sequence.

ACCESSION BF696981
VERSION BF696981.1 GI:11982389
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 719)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
Email: cgaaps@email.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
<http://image.llnl.gov>
Plate: LHCN1124 row: 9 column: 15
High quality sequence stop: 632.

FEATURES

source

Location/Qualifiers
1..719
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/clone="IMAGE:4287014"
/tissue_type="Primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH MGC 56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgccgcgcgc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGCGCGGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.: 1.49e-55 Length: 719
Score: 485.00 Matches: 97
Percent Similarity: 97.00% Conservative: 0
Best Local Similarity: 97.00% Mismatches: 1
Query Match: 93.81% Indels: 2
DB: 2 Gaps: 0

US-10-001-254-6 (1-98) x BF696981 (1-719)

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DB 92 ACATATGCGCCCTCCCTCAATGTTGACTAATTAAGAAAGCTGCATTTTATGATCCT 151
QY 21 GlnGluGlyTTPlySLysLeuAlaValAlaIleLysLysProSerGlyAaspAparGlyr 40
DB 152 CAGAAGAGATGAGAAAGATTAGCAGTCGCTATTAACCAATCTGCTGATGATATAC 211
QY 41 AaenGlnPheHsiIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrsr 60
DB 212 AATCAGTTTCACATTAAGAGATTGAAAGATTACTCAATTAAGAAAGCCCAAGTGT 271
QY 61 GluLeuLeuPheAaspTTPGlyThrThraenCysThrValGlyAaspLeuValAaspLeu 80
DB 272 GAATTACTGTTTGCATCGGGCACCAAAATTGCACAGTTTGATGATGATGATCTTTT 331
QY 80 uIlegInaenGluPhePheAlaProAlaSerLeuLeuProAaspAlaValApro 98
DB 332 GATCCAAATGAGATTGCTTTCCTCCCTGCAAGTCTTTTGTCTCCCAAGTCTGTCCC 387

RESULT 7

CA538859

LOCUS 503 bp mRNA linear EST 19-NOV-2002
DEFINITION C0272B01-5N NIA Mouse 7.5-dpc Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:C0272B01 IMAGE:30017484 5', mRNA sequence.

ACCESSION CAS38859
VERSION CA538859.1 GI:25080828
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 503)
AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Lim, M.K., Luo, A., and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other ESTs: C0272B01-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: C0272 row: B column: 01
Seq primer: M13 Reverse
High quality sequence stop: 503
POLYA=No.
Location/Qualifiers
1. .503
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="NIA:C0272B01 IMAGE:30017484"
/tissue_type="Whole embryo including extraembryonic tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of four embryos at 7.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGACGGCCCTTTTCTTTT-3'] from 7 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN
Alignment Scores:
Pred. No.: 1.56e-54 Length: 503
Score: 476.00 Matches: 89
Percent Similarity: 95.92% Conservative: 5
Best Local Similarity: 90.82% Mismatches: 4
Query Match: 92.07% Indels: 0
DB: 6 Gaps: 0
US-10-001-254-6 (1-98) x CA538859 (1-503)
Qy 1 ThrTyValAlGyCyLeuAsnValGlyLeuIleArgTyLeuSerApsPheIleApsPro 20

|||||
Db 192 ACATACATACGCAACCTTAATGTGGAGATCCTTGGAAGCTGTGAGTTATTATGATCCT 251
Qy 21 GInGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyApsApsArgTyR 40
Db 252 CAGAGAGGTGGAGAAATTTGCGATGCTTCAAAAAGCCCTCGGCGACGACGATAC 311
Qy 41 AasnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThSer 60
Db 312 AATCAGTTCCATATAGAGAGATTGGAAGCCCTTACAGACGGGGAAGACCCACCTGT 371
Qy 61 GluLeuLeuPheAapTrpGlyThrThraGlyThrValGlyApsLeuValApsLeuLeu 80
Db 372 GAACGTGCTTTGACTGGGGGACCAACGACAGTTGGCGACTTGTGATCTACTG 431
Qy 81 ILeGlnaGlnGlyPhePheAlaProAlaSerLeuLeuPProApsAlaValPro 98
Db 432 GTCCAGATTGAGCTGTTTGCCCGCCGCACTCTCTGCTGCCGAGTGCCTGCC 485
RESULT 8
LOCUS B0552228
DEFINITION H4014C09-5 NIA Mouse 7.4K cDNA clone set Mus musculus cDNA clone
LOCUS H4014C09 5', mRNA sequence.
ACCESSION B0552228
VERSION B0552228
KEYWORDS B0552228.1 GI:21453114
SOURCE EST.
ORGANISM Mus musculus (house mouse)
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 598)
AUTHORS VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Kargul, G.J., Luo, A.G., Kelso, J., Hide, N., and Ko, M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
JOURNAL Genome Res. 12 (12), 1999-2003 (2002)
MEDLINE 22354164
PUBMED 12466305
COMMENT Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html for details.
Plate: H4014 row: C column: 09
Seq primer: -21M13 Reverse
High quality sequence stop: 598
POLYA=No.
Location/Qualifiers
1. .598
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/clone_lib="NIA Mouse 7.4K cDNA clone set"
/note="Vector: pSPORT1, Site 1: SalI, Site 2: NotI. This clone is among a rearranged set of 7,407 clones from more than 20 cDNA libraries."

ORIGIN
Alignment Scores:
Pred. No.: 1.98e-54 Length: 598
Score: 476.00 Matches: 89
Percent Similarity: 95.92% Conservative: 5
Best Local Similarity: 90.82% Mismatches: 4
Qy 1 ThrTyValAlGyCyLeuAsnValGlyLeuIleArgTyLeuSerApsPheIleApsPro 20

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

source

location/Qualifiers

1..2481

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/dev_stage="10 days neonate"

116..1495

/note="unnamed protein product: interleukin-1

receptor-associated kinase 4 [Mus musculus]

putative"

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DRYNOFHIRPFALLQTKSPTECELLFDGTTNCTVGLVDLNLQELFAPATLLP

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VLSTELKQDFDQEIKVATCOHENLVLLGFSDSDNLCIVYAVMNGSLDRLSC

LDGTPPLSMHTRCVAGTANGIRPLHFNHRIHDIKSANILLDKDTAKISDFGLAR

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ORIGIN

Alignment Scores:

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Score: 476.00 Matches: 89
Percent Similarity: 95.92% Conservative: 5
Best Local Similarity: 90.82% Mismatches: 4
Query Match: 92.07% Indels: 0
DB: 3 Gaps: 0

US-10-001-254-6 (1-98) x AK028837 (1-2481)

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QY      21  GInGluGlyTyrDlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
      200 CAAGAAGGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCAGACAGATAC 259
QY      41  AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
      260 AATCAGTTCATATAAGAGATTTCGAAGCCTTACTTCAGACCGGAAAGAGCCCACTGT 319
QY      61  GluLeuLeuPheAspTyrPylThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
      320 GAACGCTGCTTGTGACCTGGGGCAACAGACTGACAGCTTGCGACCTTGTGAAATCTACTG 379
QY      81  IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
      380 GTCCAGATTGAGCTGTTGGCCCCCGCACTCTCTGCTCCGGAATGCCGTTCCC 433
DB

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Search completed: January 12, 2005, 08:51:51
Job time : 2555 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 06:32:57 ; Search time 68 Seconds
(without alignments)
791.560 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
Sequence: 1 TYVRCINLVGIRKLSDFIDP.....LLIONERFAPASLLPDAVP 98

Scoring table:
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Xgapop 10.0, Ygapext 0.5
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	833	4	US-09-166-350-10
2	517	100.0	2817	4	US-09-966-451-3
3	236	49.5	31000	4	US-09-966-451-10
4	96.5	18.7	2288	3	US-09-135-232-1
5	96.5	18.7	2288	4	US-09-863-549-1
6	79	15.3	1806	2	US-08-980-060-1
7	79	15.3	1806	2	US-08-980-060-1
8	79	15.3	1806	2	US-09-307-185-1
9	79	15.3	1806	4	US-09-773-753-1
9	79	15.3	3459	2	US-08-980-060-3
10	79	15.3	3459	3	US-09-307-185-3
11	79	15.3	3459	4	US-09-773-753-3
12	78.5	15.2	479	2	US-08-980-060-14

C 13	78.5	15.2	479	3	US-09-307-185-14	Sequence 14, Appl
C 14	78.5	15.2	479	4	US-09-773-753-14	Sequence 14, Appl
C 15	72	13.9	536165	4	US-09-214-808-1	Sequence 1, Appl
C 16	70.5	13.6	901	4	US-09-799-451-434	Sequence 43, App
17	69.5	13.4	1416	3	US-09-234-393-26	Sequence 26, Appl
18	69.5	13.4	1416	4	US-09-360-545-19	Sequence 19, Appl
19	69.5	13.4	1416	4	US-08-865-171-26	Sequence 26, Appl
20	69.5	13.4	1785	3	US-09-234-393-49	Sequence 49, Appl
21	69.5	13.4	1785	3	US-09-234-393-51	Sequence 51, Appl
22	69.5	13.4	1785	3	US-09-234-393-53	Sequence 53, Appl
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31	69.5	13.4	1977	3	US-09-234-393-23	Sequence 23, Appl
32	69.5	13.4	1977	4	US-09-865-171-23	Sequence 23, Appl
33	66.5	12.9	265	4	US-09-313-284A-3660	Sequence 3660, Ap
34	66.5	12.9	648	4	US-09-489-039A-5677	Sequence 5677, Ap
35	66	12.8	213	4	US-09-248-796A-7045	Sequence 7045, Ap
36	66	12.8	837	4	US-09-248-796A-2167	Sequence 2167, Ap
37	66	12.8	987	4	US-09-252-991A-11251	Sequence 11251, A
38	66	12.8	1140	4	US-09-252-991A-11181	Sequence 11181, A
C 39	66	12.8	3141	4	US-09-252-991A-10937	Sequence 10937, A
C 40	65	12.6	547	4	US-09-854-133-306	Sequence 306, App
C 41	65	12.6	1623	4	US-09-513-783A-33	Sequence 33, Appl
C 42	65	12.6	1623	4	US-09-430-656-33	Sequence 33, Appl
C 43	64.5	12.5	1521	3	US-09-134-001C-470	Sequence 470, App
C 44	64.5	12.5	1989	4	US-09-534-228B-6	Sequence 6, Appl
C 45	64.5	12.5	4066	4	US-09-710-279-4327	Sequence 4327, Ap

ALIGNMENTS

RESULT 1
US-09-166-350-10
; Sequence 10, Application US/09166350A
; Patent No. 6440663

GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-166-350-10

Alignment Scores:

Pred. No.: 3.96e-72

Score: 517.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 4

Gaps: 0

US-10-001-254-6 (1-98) x US-09-166-350-10 (1-833)

Length: 833

Matches: 98

Conservative: 0

Mismatches: 0

Indels: 0

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QY 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 134 CAAGAGAGATGAGAAAGATTAGCTGATGCTATTAATAAACCATCTGGTGAATGATGATAC 193
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACTAAGAGATTGAGATTAAGCATTAATTCAAACTGGAAGAAAGTCCACTTCT 253
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Db 254 GAATTAAGTGTGAGCTGGGACCAAAATTGACAGTTGGTGTATCTTGTGATCTTTTG 313
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
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RESULT 2
US-09-966-451-3
; Sequence 3, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1432)
US-09-966-451-3

Alignment Scores:
Pred. No.: 2,566-71 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-10-001-254-6 (1-98) x US-09-966-451-3 (1-2817)
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Db 134 CAAGAGAGATGAGAAAGATTAGCTGATGCTATTAATAAACCATCTGGTGAATGATGATAC 193
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Db 194 AATCAGTTTCACTAAGAGATTGAGATTAAGCATTAATTCAAACTGGAAGAAAGTCCACTTCT 253
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCystrValGlyAspLeuValAspLeuLeu 80
Db 254 GAATTAAGTGTGAGCTGGGACCAAAATTGACAGTTGGTGTATCTTGTGATCTTTTG 313
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 314 ATCCAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 3
US-09-966-451-10
```

```
; Sequence 10, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-966-451-10

Alignment Scores:
Pred. No.: 2,686-28 Length: 31000
Score: 256.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
Gaps: 0
DB: 4

US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)
QY 45 IleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGlyLeuPhe 64
Db 12963 TTAAGAGATTTGAAGCATTAATCAAACTGAAAGAAAGTCCACTTGAATTAATGTTT 13022
QY 65 AspTTPGlyThrThrAsnCystrValGlyAspLeuValAspLeuLeuIleGlnAsnGln 84
Db 13023 GACTGGGACCAACAAATTGACAGTTGATCTTGTGATTCCTTGAATCAAAATGAA 13082
QY 85 PhePheAlaProAlaSerLeuLeuLeuPro 94
Db 13083 TTTTGTCTCTCGAGATCTTTGTCTCCA 13112

RESULT 4
US-09-135-232-1
; Sequence 1, Application US/09135232
; Patent No. 6262228
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: T98-019
; CURRENT APPLICATION NUMBER: US/09/135,232
; CURRENT FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2288
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1851)
US-09-135-232-1

Alignment Scores:
Pred. No.: 0,000102 Length: 2288
Score: 96.50 Matches: 23
Percent Similarity: 47.95% Conservative: 12
Best Local Similarity: 31.51% Mismatches: 31
Query Match: 18.67% Indels: 7
Gaps: 1
DB: 3

US-10-001-254-6 (1-98) x US-09-135-232-1 (1-2288)
QY 8 ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTTPylsLysLeu 27
Db 136 CTCGAGAGCTTCGCCGCTGTTCTGACAGCTGACGCGCGCTGCGCTGCGCGCTG 195
```

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Qy 28 AlaValAlaIleIleValysProSerGlyAspAspArgTyrAnGlnPheHisIleAlaArg 47
Db 196 GCAGAGAGACTTTCAGC-----ACCTGAGCTGATGTTCTCAT 234
Qy 48 PheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuPheAspTyrGly 67
Db 235 ATTGAAGAAGTGTGAGCCAAAGTAAAGTGAACAGAAATTAATTGCTCTGGGCA 294
Qy 68 ThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
Db 295 CAGAAAAACAAGACCATCGTGACCTTTACAGGCTCTC 333

RESULT 5
US-09-863-549-1
; Sequence 1, Application US/09863549
; Patent No. 6576444
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: 198-019
; CURRENT APPLICATION NUMBER: US/09/863,549
; PRIOR FILING DATE: 2001-05-22
; PRIORITY APPLICATION NUMBER: 09/135,232
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2288
; TYPE: DNA
; ORGANISM: human
; NAME/KEY: CDS
; LOCATION: (64)..(1851)
; US-09-863-549-1

Alignment Scores:
Pred. No.: 0.000102 Length: 2288
Score: 96.50 Matches: 23
Percent Similarity: 47.95% Conservative: 12
Best Local Similarity: 31.51% Mismatches: 31
Query Match: 18.67% Indels: 7
DB: Gaps: 1

US-10-001-254-6 (1-98) x US-09-863-549-1 (1-2288)
Qy 8 ValGlyLeuIleArgGlyLysSerAspPheIleAspProGlnGluGlyTyrLysLeu 27
Db 136 CTCGGAGAGCTCGCGCTGTTCTGGAACAGCTGCAGCGCGGCTGGCGGCGCTG 195
Qy 28 AlaValAlaIleIleValysProSerGlyAspAspArgTyrAnGlnPheHisIleAlaArg 47
Db 196 GCAGAGAGACTTTCAGC-----ACCTGAGCTGATGTTCTCAT 234
Qy 48 PheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuPheAspTyrGly 67
Db 235 ATTGAAGAAGTGTGAGCCAAAGTAAAGTGAACAGAAATTAATTGCTCTGGGCA 294
Qy 68 ThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
Db 295 CAGAAAAACAAGACCATCGTGACCTTTACAGGCTCTC 333

RESULT 6
US-08-980-060-1
; Sequence 1, Application US/08980060
; Patent No. 5965421
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: FENG, PING
; APPLICANT: MUZIO, MARTA
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,060
; FILING DATE: Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/ALX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1806 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..1803
; US-08-980-060-1

Alignment Scores:
Pred. No.: 0.0423 Length: 1806
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
DB: Gaps: 2

US-10-001-254-6 (1-98) x US-08-980-060-1 (1-1806)
Qy 45 IleArgArgPheGluAlaLeuGlnThr---GlyLysSerProThrSerGluLeuLeu 63
Db 157 CTCGGAAGATCAAGTCATGAGCGGATGCAAGGTGTGAGCATCAGCGGAGCTGCTG 216
Qy 64 PheAspTyrGlyThrThrAnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsn 83
Db 217 TGGTGTGGGGCATGCGGCGAGGCCACCGTCACGAACTTGTGACCTCTGTGCGGCTG 276
Qy 84 GluPhePheAlaProIleSerLeuLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCCAGATCATCTGAATCGAACCAGGCTCTGAATCAGGTGT 336
Qy 94 -----ProAspAlaVal 97
Db 337 CCCATTCAGGCTTCCCTGACTGTGTG 363

RESULT 7
US-09-307-185-1
; Sequence 1, Application US/09307185
; Patent No. 6222019
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: FENG, PING
; APPLICANT: MUZIO, MARTA
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,185
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,060
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1806 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..1803
; US-09-307-185-1

Alignment Scores:
Pred. No.: 0.0423 Length: 1806
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
DB: 3 Gaps: 2

US-10-001-254-6 (1-98) x US-09-307-185-1 (1-1806)
QY 45 IleaTgATgPheGluAlaLeuLeuGlnThr---GLYSeSerProthrsErgIleuLeu 63
Db 157 CTGCGGAAGATCAAGTCCATCGAGCGGAGGTGTAGCATCAACGCGGAGCTGTG 216
QY 64 PheaSpTPGlyThrThraaNCythrValGlyAspLeuValAspLeuLeuIleGlnaen 83
Db 217 TGGGTGTGGGCGATCGGCGAGCCACCGTCAGCAACTTGTGACTCTGTGCGCCGTG 276
QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCCAGATCATCTGAAGTGAACCGGCTCTGAAATCAGGTGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCCTTCCCTGACTCTGTG 363

RESULT 8
US-09-773-753-1
; Sequence 1, Application US/09773753
; Patent No. 6653452
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; PENG, PING
; MUZIO, MARTA
; DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2

```

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/773,753
; FILING DATE: 02-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/980,060
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1806 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..1803
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-773-753-1

Alignment Scores:
Pred. No.: 0.0423 Length: 1806
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
DB: 4 Gaps: 2

US-10-001-254-6 (1-98) x US-09-773-753-1 (1-1806)
QY 45 IleaTgATgPheGluAlaLeuLeuGlnThr---GLYSeSerProthrsErgIleuLeu 63
Db 157 CTGCGGAAGATCAAGTCCATCGAGCGGAGGTGTAGCATCAACGCGGAGCTGTG 216
QY 64 PheaSpTPGlyThrThraaNCythrValGlyAspLeuValAspLeuLeuIleGlnaen 83
Db 217 TGGGTGTGGGCGATCGGCGAGCCACCGTCAGCAACTTGTGACTCTGTGCGCCGTG 276
QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCCAGATCATCTGAAGTGAACCGGCTCTGAAATCAGGTGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCCTTCCCTGACTCTGTG 363

RESULT 9
US-08-980-060-3
; Sequence 3, Application US/08980060
; Patent No. 5965421
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; PENG, PING

```

APPLICANT: MUZIO, MARTA
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
US-08-980-060-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
US-10-001-254-6 (1-98) x US-08-980-060-3 (1-3459)
Qy 45 IleaRgArPheGuaAlaLeuLeuGlnThr---GlyLySerProThrSerGluLeuLeu 63
Db 157 CTGGGAGAGATCAAGTCATGAGCGGGGTGAGCAGATCACCGGAGACTGCTG 216
Qy 64 PheaSPTpGlyThrThrAnCysThrValGlyAspleuValAspleuLeuIleGlnAsn 83
Db 217 TGGGTGTGGGGCAGTGGCGGACGCGCTCCAGCAACTTGTGAGCTCTGTGCGCGCTG 276
Qy 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCGCAGATCATCTGAATCGAAGAACCGGCTCTGAATCAGGTGT 336
Qy 94 -----ProAspAlaVal 97
Db 337 CCATTCACGCTTCCTGACTCTGTG 363
RESULT 10
US-09-307-185-3
Sequence 3, Application US/09307185
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: PENG, PING
APPLICANT: MUZIO, MARTA

APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,185
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
US-09-307-185-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
US-10-001-254-6 (1-98) x US-09-307-185-3 (1-3459)
Qy 45 IleaRgArPheGuaAlaLeuLeuGlnThr---GlyLySerProThrSerGluLeuLeu 63
Db 157 CTGGGAGAGATCAAGTCATGAGCGGGGTGAGCAGATCACCGGAGACTGCTG 216
Qy 64 PheaSPTpGlyThrThrAnCysThrValGlyAspleuValAspleuLeuIleGlnAsn 83
Db 217 TGGGTGTGGGGCAGTGGCGGACGCGCTCCAGCAACTTGTGAGCTCTGTGCGCGCTG 276
Qy 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCGCAGATCATCTGAATCGAAGAACCGGCTCTGAATCAGGTGT 336
Qy 94 -----ProAspAlaVal 97
Db 337 CCATTCACGCTTCCTGACTCTGTG 363
RESULT 11
US-09-773-753-3
Sequence 3, Application US/09773753
GENERAL INFORMATION:
APPLICANT: NI, JIAN

FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,060
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AMK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-773-753-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
US-10-001-254-6 (1-98) x US-09-773-753-3 (1-3459)
QY 45 IleaTgAgPheGluAlaLeuLeuGlnThr---GlyVLeSerProThrSerGluLeuLeu 63
Db 157 CTGCGGAAGATCAAGTCCATGAGCGGCGTGCAGGGGTGAGCATCAAGCGGAGAGCTGCTG 216
QY 64 PheaApTtPglYThrThraAnCyethrValGlyAspLeuValAspLeuLeuLeuLeu 83
Db 217 TGTGTGTGGGGCATGCGGAGCGCACCGTCCAGCAACTTGTGAGCCTCTGTGCGCGCTG 276
QY 84 GluPhePheAlaProAlaSerLeuLeuLeu----- 93
Db 277 GAGCTCTACCGGGCTCCAGATCACTCCAGACTGGAAACCGGCTCTGTAATCATGATGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCTTCCCTGACTCTGTG 363
RESULT 12
US-08-980-060-14/c
Sequence 14, Application US/08980060

Patent No. 5965421
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AMK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-980-060-14
Alignment Scores:
Pred. No.: 0.00664 Length: 479
Score: 78.50 Matches: 19
Percent Similarity: 60.00% Conservative: 11
Best Local Similarity: 38.00% Mismatches: 19
Query Match: 15.18% Indels: 1
Gaps: 1
US-10-001-254-6 (1-98) x US-08-980-060-14 (1-479)
QY 45 IleaTgAgPheGluAlaLeuLeuGlnThr---GlyVLeSerProThrSerGluLeuLeu 63
Db 244 CTGCGGAAGATCAAGTCCATGAGCGGCGTGCAGGGGTGAGCATCAAGCGGAGAGCTGCTG 185
QY 64 PheaApTtPglYThrThraAnCyethrValGlyAspLeuValAspLeuLeuLeuLeu 83
Db 184 TGTGTGTGGGGCATGCGGAGCGCACCGTCCAGCAACTTGTGAGCCTCTGTGCGCGCTG 125
QY 84 GluPhePheAlaProAlaSerLeuLeuLeu----- 93
Db 124 GAGCTCTACCGGGCTCCAGATCACTCCAGACTGGAAACCGGCTCTGTAATCATGATGT 95
RESULT 13
US-09-307-185-14/c
Sequence 14, Application US/09307185
Patent No. 6222019
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/307,185
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/980,060
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STERRE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 479 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-09-307-185-14

Alignment Scores:
Pred. No.: 0.00664 Length: 479
Score: 78.50 Matches: 19
Percent Similarity: 60.00% Conservative: 11
Best Local Similarity: 38.00% Mismatches: 19
Query Match: 15.18% Indels: 1
Gaps: 1
DB: 3

US-10-001-254-6 (1-98) x US-09-307-185-14 (1-479)

QY 45 IleaRgArpGheGuaAlaLeuLgInThr---GlyLySeRProThrSerGluLeuLeu 63
:::||||: :||||: :|||
Db 244 CTGCGGAAGATCAAGTCATGAGCGGCTGCAGCGGTGAGCATCACCGCGAGCTGCTG 185
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QY 64 PheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuIleGlnAsn 83
:::||||: :||||: :|||
Db 184 TGGTGTGTGGGGCAGCGCGAGCCACCGTCCAGCAACTTGTGACCTCTGTGCGGCTG 125
:::||||: :||||: :|||

QY 84 GluPheheAlaProAlaSerLeuLeu 93
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Db 124 GAGCTTAACGGCGCTGCCAGATCATCTG 95
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RESULT 14
US-09-773-753-14/c
; Sequence 14, Application US/09773753
; Patent No. 6653452
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; FENG, PING
; MUZIO, MARTA
; DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.

;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/773,753
;; FILING DATE: 02-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/980,060
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STERRE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 479 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
;; US-09-773-753-14

Alignment Scores:
Pred. No.: 0.00664 Length: 479
Score: 78.50 Matches: 19
Percent Similarity: 60.00% Conservative: 11
Best Local Similarity: 38.00% Mismatches: 19
Query Match: 15.18% Indels: 1
Gaps: 1
DB: 4

US-10-001-254-6 (1-98) x US-09-773-753-14 (1-479)

QY 45 IleaRgArpGheGuaAlaLeuLgInThr---GlyLySeRProThrSerGluLeuLeu 63
:::||||: :||||: :|||
Db 244 CTGCGGAAGATCAAGTCATGAGCGGCTGCAGCGGTGAGCATCACCGCGAGCTGCTG 185
:::||||: :||||: :|||

QY 64 PheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuIleGlnAsn 83
:::||||: :||||: :|||
Db 184 TGGTGTGTGGGGCAGTCGCGAGCCACCGTCCAGCAACTTGTGACCTCTGTGCGGCTG 125
:::||||: :||||: :|||

QY 84 GluPheheAlaProAlaSerLeuLeu 93
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Db 124 GAGCTTAACGGCGCTGCCAGATCATCTG 95
||| :||| :|||

RESULT 15
US-09-214-808-1
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; Patent No. 6475793
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/214,808A
; CURRENT FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/IB97/00950
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1

LENGTH: 536165
 TYPE: DNA
 ORGANISM: Rhizobium
 US-09-214-808-1

Alignment Scores:

Pred. No.:	3.37e+03	Length:	536165
Score:	72.00	Matches:	28
Percent Similarity:	47.06%	Conservative:	12
Best Local Similarity:	32.94%	Mismatches:	39
Query Match:	13.93%	Indels:	6
DB:	4	Gaps:	5

US-10-001-254-6 (1-98) x US-09-214-808-1 (1-536165)

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QY 18 11leasprogingiuglytrp--lyslslsleualavalalallelyslsProSer--- 35
    |||||.....|||.....|
DB 97239 ATGACGATCGGGGAGCTTGGGACAGAGAAATCAGTTGCTGCTCAACGTCCTGCC 97298
    |||||.....|
QY 36 ---GlyAspAspArg--TyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeuGln 53
    |||||.....|
DB 97299 ACCGGCGATGACATCTGACTTGGCTCCCTGCAGATCCACGATATATCAATCTTGTTAG 97358
    |||||.....|
QY 54 ThrGlyLysSerProthrSerGluLeuLeuPheAspTyrGlyThrThrAsnQystrVal 73
    |||||.....|
DB 97359 ATTAGGCTTCGGCTCACTTAGATGCTTCTTGATG---TCTACTAACTGGCCTCAA 97415
    |||||.....|
QY 74 ---GlyAspLeuValAspLeuLeuIleGlnAsnGlnPhePheAlaProIaSerLeuLeu 92
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DB 97416 TGAAGTGACTTACAGCGCGCTTTCCAATCCGCTTCTTATCCGCTCTTCAAAATG 97475
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QY 93 LeuProAspAlaVal 97
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DB 97476 GTGCAATCAATGTT 97490
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Search completed: January 12, 2005, 08:54:30
 Job time : 157 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 05:41:00 ; Search time 3301 Seconds

(without alignments)

1403.935 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
Sequence: 1 TYVRCINVGIRKLSDFIDP.....LLIONEPFAPASLLPNAVP 98

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.spool/h/US10001254/runac_10012005_172738_10459/app_query.fasta_1.263
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-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEDBPRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MANY_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmb1: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
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12: gb_by: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	100.0	294	AX431296	Sequence
2	517	100.0	833	AR223870	Sequence
3	517	100.0	1383	AX431306	Sequence
4	517	100.0	1629	BC013316	Homo sapi

5	517	100.0	1636	9	AY340962	AY340962 Homo sapi
6	517	100.0	1684	9 <th>AY340963</th> <th>AY340963 Homo sapi</th>	AY340963	AY340963 Homo sapi
7	517	100.0	2775	6 <th>CO728380</th> <th>CO728380 Sequence</th>	CO728380	CO728380 Sequence
8	517	100.0	2817	6 <th>AR475548</th> <th>AR475548 Sequence</th>	AR475548	AR475548 Sequence
9	517	100.0	2817	6 <th>AX431318</th> <th>AX431318 Sequence</th>	AX431318	AX431318 Sequence
10	517	100.0	2817	6 <th>AF155118</th> <th>AF155118 Homo sapi</th>	AF155118	AF155118 Homo sapi
11	517	100.0	2820	9 <th>AK000528</th> <th>AK000528 Homo sapi</th>	AK000528	AK000528 Homo sapi
12	513	99.2	1381	9 <th>AY283671</th> <th>AY283671 Homo sapi</th>	AY283671	AY283671 Homo sapi
13	513	99.2	1383	6 <th>AX196260</th> <th>AX196260 Sequence</th>	AX196260	AX196260 Sequence
14	513	99.2	1383	9 <th>AF445802</th> <th>AF445802 Homo sapi</th>	AF445802	AF445802 Homo sapi
15	513	99.2	1383	9 <th>AY283670</th> <th>AY283670 Homo sapi</th>	AY283670	AY283670 Homo sapi
16	478	92.5	1703	9 <th>AY340966</th> <th>AY340966 Homo sapi</th>	AY340966	AY340966 Homo sapi
17	478	92.5	1751	9 <th>AY340967</th> <th>AY340967 Homo sapi</th>	AY340967	AY340967 Homo sapi
18	476	92.1	1542	6 <th>AX196262</th> <th>AX196262 Sequence</th>	AX196262	AX196262 Sequence
19	476	92.1	1542	10 <th>AF445803</th> <th>AF445803 Mus muscu</th>	AF445803	AF445803 Mus muscu
20	476	92.1	2431	10 <th>BC051676</th> <th>BC051676 Mus muscu</th>	BC051676	BC051676 Mus muscu
21	413	79.9	501	6 <th>AX321132</th> <th>AX321132 Sequence</th>	AX321132	AX321132 Sequence
22	287	55.5	1452	5 <th>AY616584</th> <th>AY616584 Danio rer</th>	AY616584	AY616584 Danio rer
23	287	55.5	1719	5 <th>BC045381</th> <th>BC045381 Danio rer</th>	BC045381	BC045381 Danio rer
24	256	49.5	31000	6 <th>AR475555</th> <th>AR475555 Sequence</th>	AR475555	AR475555 Sequence
25	256	49.5	33033	9 <th>AY186092</th> <th>AY186092 Homo sapi</th>	AY186092	AY186092 Homo sapi
26	256	49.5	118572	9 <th>AC093012</th> <th>AC093012 Homo sapi</th>	AC093012	AC093012 Homo sapi
27	256	49.5	165868	2 <th>AC021719</th> <th>AC021719 Homo sapi</th>	AC021719	AC021719 Homo sapi
28	256	49.5	309582	2 <th>AC025567</th> <th>AC025567 Homo sapi</th>	AC025567	AC025567 Homo sapi
29	247	47.8	211	6 <th>AX431316</th> <th>AX431316 Sequence</th>	AX431316	AX431316 Sequence
30	247	47.8	470	6 <th>CO681170</th> <th>CO681170 Sequence</th>	CO681170	CO681170 Sequence
31	247	47.8	1490	9 <th>AY340964</th> <th>AY340964 Homo sapi</th>	AY340964	AY340964 Homo sapi
32	247	47.8	1538	9 <th>AY340965</th> <th>AY340965 Homo sapi</th>	AY340965	AY340965 Homo sapi
33	247	47.8	1781	9 <th>AK027301</th> <th>AK027301 Homo sapi</th>	AK027301	AK027301 Homo sapi
34	247	47.8	2213	6 <th>AX875837</th> <th>AX875837 Sequence</th>	AX875837	AX875837 Sequence
35	247	47.8	2213	6 <th>BD155790</th> <th>BD155790 Primer fo</th>	BD155790	BD155790 Primer fo
36	233	45.1	264657	2 <th>AC129390</th> <th>AC129390 Rattus no</th>	AC129390	AC129390 Rattus no
37	230	44.5	205374	10 <th>AC147160</th> <th>AC147160 Mus muscu</th>	AC147160	AC147160 Mus muscu
38	123	23.8	736	11 <th>BV075713</th> <th>BV075713 S212P6044</th>	BV075713	BV075713 S212P6044
39	121.5	23.5	2069	3 <th>AK116443</th> <th>AK116443 Ciona int</th>	AK116443	AK116443 Ciona int
40	98.5	19.1	1730	10 <th>MMU440757</th> <th>MMU440757 Mus muscu</th>	MMU440757	MMU440757 Mus muscu
41	96.5	18.7	1891	6 <th>AX056430</th> <th>AX056430 Sequence</th>	AX056430	AX056430 Sequence
42	96.5	18.7	1891	9 <th>BC069388</th> <th>BC069388 Homo sapi</th>	BC069388	BC069388 Homo sapi
43	96.5	18.7	2277	6 <th>AX057324</th> <th>AX057324 Sequence</th>	AX057324	AX057324 Sequence
44	96.5	18.7	2288	6 <th>AR342634</th> <th>AR342634 Sequence</th>	AR342634	AR342634 Sequence
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ALIGNMENTS

RESULT 1
AX431296 LOCUS 294 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 5 from Patent WO0240680.
ACCESSION AX431296
VERSION AX431296.1 GI:21656165
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S. H., Reed, J. C.,
Roch, W. and Stenner-Liawen, F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240680-A 5 23-MAY-2002;
BURNHAM INST (US)
FEATURES
Source
1..294
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..>294
/note="unassigned protein product"
/codon_start=1
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/db_xref="GI:21656166"
/translation="TYVRCINVGIRKLSDFIDPQEGMKLAVAIKKPSGDDRYNQPH"

ORIGIN IRRPALLQTKSPSTSEILFDMGTNCTVGBLVLDLIQNEFPAPASILLPDVAP"

Alignment Scores:

Pred. No.: 1.4e-61 Length: 294

Score: 517.00 Matches: 98

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AX431296 (1-294)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20

DB 1 ACATATGCGCGCTCCCAATGTTGACTAATAGAGAGCTGACATTTTATGATCCT 60

QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsPProSerGlyAspAspArgTyr 40

DB 61 CAAGAAAGATGAGAAAGATTAGCTGATGCTATTTAAAAACCATCTGCTGATGATGATAC 120

QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyIysSerProThrSer 60

DB 121 AATCAGTTTCACTAAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCATCTT 180

QY 61 GlnLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

DB 181 GAATTACTGTTTACTGCGGACCAACAATTGACAGATGCTGATCTTGTGGATCTTTTG 240

QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

DB 241 ATCCAAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTTCCC 294

RESULT 2

LOCUS AR223870 833 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 10 from patent US 6440663.

ACCESSION AR223870

VERSION AR223870.1 GI:23332452

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 833)

AUTHORS Scanlan,M.J., Stockert,E., Chen,Y.-T., Old,L.J., Jager,E. and Knuth,A.

TITLE Renal cancer associated antigens and uses therefor

JOURNAL Patent: US 6440663-A 10 27-AUG-2002;

FEATURES

location/Qualifiers

1..833

source /organism="unknown"

/mol_type="genomic DNA"

ORIGIN

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Pred. No.: 4.94e-61 Length: 833

Score: 517.00 Matches: 98

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

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QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20

DB 74 ACATATGCGCGCTCCCAATGTTGACTAATAGAGAGCTGACATTTTATGATCCT 133

QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsPProSerGlyAspAspArgTyr 40

DB 134 CAAGAAAGATGAGAAAGATTAGCTGATGCTATTTAAAAACCATCTGCTGATGATGATAC 193

QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyIysSerProThrSer 60

DB 194 AATCAGTTTCACTAAGAGATTTGAAGCATTTCAACATGAGAAAAAGTCCCATCTCT 253

QY 61 GlnLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

DB 254 GAATTACTGTTTACTGCGGACCAACAATTGACAGATGCTGATCTTGTGGATCTTTTG 313

QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

DB 314 ATCCAAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTTCCC 367

RESULT 3

LOCUS AX431306 1383 bp DNA linear PAT 28-JUN-2002

DEFINITION Sequence 15 from Patent WO0240680.

ACCESSION AX431306

VERSION AX431306.1 GI:21656175

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C., Roth,W. and Stenner-Liewen,F.

TITLE Novel death domain proteins

JOURNAL Parent: WO 0240680-A 15 23-MAY-2002;

BURNHAM INST (US)

FEATURES

location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

1..1383

/note="unamed protein product"

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ORIGIN

Alignment Scores:

Pred. No.: 9.14e-61 Length: 1383

Score: 517.00 Matches: 98

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AX431306 (1-1383)

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DB 25 ACATATGCGCGCTCCCAATGTTGACTAATAGAGAGCTGACATTTTATGATCCT 84

QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsPProSerGlyAspAspArgTyr 40

DB 85 CAAGAAAGATGAGAAAGATTAGCTGATGCTATTTAAAAACCATCTGCTGATGATGATAC 144

QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyIysSerProThrSer 60

DB 145 AATCAGTTTCACTAAGAGATTTGAAGCATTTACTTCAAACTGAGAAAAAGTCCCATCTCT 204

QY 61 GlnLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

Db	Qy	Db	RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
205	GAATTAAGCTTTGACTGGGAGCACCACAAATTCAGATGGATGATCTTGAGACTTTTG	266										
81	IIleGIanGcIuphePheAlaProAlaSerLeuLeuPProaAPhAlaValPro	98										
265	ATCCAAATGATGATTTTGTCTTCGCGAGTCTTTGTGCTCCACGATGCTGTTCC	318										
BC013316	1629 bp	mRNA	linear	PRI 30-JUN-2004								
Homo sapiens	interleukin-1 receptor-associated kinase 4, mRNA (CDNA											
clone MGC:13330 IMAGE:4287014), complete cds.												
BC013316												
BC013316	GI:15426431											
MGC												
Homo sapiens (human)												
Homo sapiens												
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.												
1 (bases 1 to 1629)												
Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,												
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,												
Altschul, S.F., Zeeberg, B., Bietow, K.H., Schaefer, C.F., Bhat, N.K.,												
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,												
Ditschenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,												
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,												
Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Tokuyuki, S.,												
Carninci, P., Prange, C., Rhee, S.S., Loquellano, N.A., Peters, G.J.,												
Abraham, R.D., Malley, S.J., Bosak, S.A., McEwan, P.J.,												
McEman, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,												
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,												
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,												
Falley, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,												
Bouchard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,												
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,												
Butterfield, Y.S., Krzywicki, M.I., Skalka, U., Smalus, D.E.,												
Schmeh, A., Schein, J.E., Jones, S.J., and Warr, M.A.												
Generation and initial analysis of more than 15,000 full-length												
human and mouse cDNA sequences												
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)												
12477932												
2 (bases 1 to 1629)												
Strauberg, R.												
Direct Submission												
Gene Collection (31-AUG-2001) National Institutes of Health, Mammalian												
Gene Collection (MGC), Cancer Genomics Office, National Cancer												
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,												
USA												
NIH-MGC Project URL: http://mgc.nci.nih.gov												
Contact: MGC help desk												
Email: cgabbs-remail.nih.gov												
Tissue Procurement: ATCC												
CDNA Library Preparation: Clontech Laboratories, Inc.												
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)												
DNA Sequencing by: Institute for Systems Biology												
http://www.systemsbio.org												
contact: amadon@systemsbio.org												

gene

CDs

US-10-001-254-6 (1-98) x BC013316 (1-1629)

Alignment Scores:

Pred. No.:	1,11e-60	Length:	1629
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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VDITBELKQOPDOEIRYMAKCOHENVELLGSSDSDILCLVYVWPKISDLRISC
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RESULT 5
AY340962 LOCUS 1636 bp mRNA linear PRI 01-AUG-2004
DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4)
ACCESSION AY340962
VERSION AY340962.1
KEYWORDS GI:13727958
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1636)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1636)

AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
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65. 1448
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LDGTPPLSMWRCKIAQGANGLNFIENHHIRDIKSANILDEAFKIDFGILAR
ASEKPAQIVMTSRIVGTATYMAPEALRGHITPKSDIYSFGVLLRITGLPVDHRE
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QQLQEMTAS"

gene
CDS
1. 126-60
517.00
100.00%
100.00%
100.00%
9
Length: 1636
Matches: 98
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

ORIGIN

Alignment Scores:
Pred. No.: 1. 126-60 Length: 1636
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY340962 (1-1636)

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Db 90 ACATATGGCGCTGCTCAATGTTGACATTAATGAGACCTGCAATTTTATGATCCT 149
QY 21 GlnGlnGlyTrrPylsLeuAlaValAlailelylsPserGlyAspAspArgTyr 40
Db 150 CAAGAAGATGAGAGAGTACTGAGCTATTAATAAACCATCTGGTATGATGATAC 209
QY 41 AenglnPheHisileArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 210 AATCGATTTCACATAGAGATTTGAGCATTAATCAATGAGAAAGTCCCACTTCT 269
QY 61 GluLeuLeuPheAspTrrPylsThrThrAsnGlyValGlyAspLeuValAspLeu 80
Db 270 GAATTAAGTGTGACCTGGGCGACCAAAATGCAAGTGGATCTTGATCTTTTG 329
QY 81 IleglnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 330 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCC 383

RESULT 6
LOCUS AY340963 1684 bp mRNA linear PRI 01-AUG-2004
DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4 variant
ACCESSION AY340963
VERSION AY340963.1 GI:37727960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 1684)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 1684)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
source
1. 1684
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1. 1684
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114. 1496
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variant"
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DAVPKTAATLPSEKALITVOOKMPFCDKRTMTVPONLEQSYMPDSSPENKSLV
SDTRPHSFEYELKNVTNNFDERPISVGKMGEGGVYKGYNNITVAAYKLAAM
VDITTEELKQDFDEIKVAKCOHENLVELGSSDGDCLIVYVMPGSLDRLSC
LDGTPPLSMWRCKIAQGANGLNFIENHHIRDIKSANILDEAFKIDFGILAR
ASEKPAQIVMTSRIVGTATYMAPEALRGHITPKSDIYSFGVLLRITGLPVDHRE
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gene
CDS
1. 166-60
517.00
100.00%
100.00%
100.00%
9
Length: 1684
Matches: 98
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

ORIGIN

Alignment Scores:
Pred. No.: 1. 166-60 Length: 1684
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY340963 (1-1684)

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QY 21 GlnGlnGlyTrrPylsLeuAlaValAlailelylsPserGlyAspAspArgTyr 40
Db 198 CAAGAAGATGAGAGAGTACTGAGCTATTAATAAACCATCTGGTATGATGATAC 257
QY 41 AenglnPheHisileArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 258 AATCGATTTCACATAGAGATTTGAGCATTAATCAATGAGAAAGTCCCACTTCT 317
QY 61 GluLeuLeuPheAspTrrPylsThrThrAsnGlyValGlyAspLeuValAspLeu 80
Db 318 GAATTAAGTGTGACCTGGGCGACCAAAATGCAAGTGGATCTTGATCTTTTG 377
QY 81 IleglnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 378 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCC 431

RESULT 7
LOCUS CQ728380 2775 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14314 from Patent WO02068579.

ACCESSION CQ728380
VERSION CQ728380.1 GI:42297030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 14314 06-SEP-2002;
PE Corporation (NY) (US)

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ORIGIN

Alignment Scores:
Pred. No.: 2,13e-60 Length: 2775
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x CQ728380 (1-2775)

Qy 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
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Qy 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 96 CAAGAAGATGGAAGAGATTAGCTGTGCTATTAACCAACATCTGCGATGATAGATAC 155

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 156 AATCAGTTTCACATAGAGATTTGAGCATTAATTCAAACTGGAAAAAGTCCACATCTCT 215

Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 216 GAATTACTGTTTGACTGGGCGACCAAAATGACAGATTGGATCTTGTGATCTTTTG 275

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 276 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 329

RESULT 8
AR475548 2817 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 3 from patent US 6692959.
DEFINITION AR475548
ACCESSION AR475548
VERSION AR475548.1 GI:42715031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2817)
AUTHORS Bennett, C.F. and Freier, S.M.
TITLE Antisense modulation of IL-1 receptor-associated kinase-4
expression
JOURNAL Patent: US 6692959-A 3 17-FEB-2004;
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source
1..2817
Location/Qualifiers
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x AR475548 (1-2817)

Qy 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
Db 74 ACATATGCGCGCTCCCTCAATGTGAGCTAATTAGGAAGCTGTCAAGATTATTAATGATCCT 133

Qy 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 134 CAAGAAGATGGAAGAGATTAGCTGTGCTATTAACCAACATCTGCGATGATAGATAC 193

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACATAGAGATTTGAGCATTAATTCAAACTGGAAAAAGTCCACATCTCT 253

Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 254 GAATTACTGTTTGACTGGGCGACCAAAATGACAGATTGGATCTTGTGATCTTTTG 313

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 367

RESULT 9
AX431318 2817 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 27 from Patent WO0240680.
DEFINITION AX431318
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,
Roch, W. and Steiner-Weber, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
BURNHAM INST (US)

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Location/Qualifiers
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/db_xref="GI:21656188"

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ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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Qy 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 134 CAAGAAGATGGAAGAGATTAGCTGTGCTATTAACCAACATCTGCGATGATAGATAC 193

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACATAGAGATTTGAGCATTAATTCAAACTGGAAAAAGTCCACATCTCT 253

Qy 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 254 GAATTACTGTTTGACTGGGCGACCAAAATGACAGATTGGATCTTGTGATCTTTTG 313

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 367

RESULT 9
AX431318 2817 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 27 from Patent WO0240680.
DEFINITION AX431318
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,
Roch, W. and Steiner-Weber, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
BURNHAM INST (US)

FEATURES
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50..1432
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD37285.1"
/db_xref="GI:21656188"

CDs
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DAVKNANTLPSKEALITVQOKMPFCDKRRLMTPTVONLEOSYMPDSSSPBKSLSEV
SDTRFHSFSEYELKVNNTNDEPRLISVGKMGEGGGVYKGVNNTVAVKGLAM
VDITTEELKQDFDEIKVMKCOHBNVELGFSPOGDDCLVYVYVNPNGSLDLRLSC
LDGTPPLSMRCKIAAGANGINFLHNNHHRDIKSNILIDEPATKISDPLGRLAR
ASKEPQATVNTSRIVGTATMAPEALRGELTPSDYISFVVLLEITITGIPAYDEHRE
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HOLIOEWNTAS"

ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AK431318 (1-2817)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgTysLeuSerAspPheIleAspPro 20
 DB 74 ACATATGTCGCGCTCAATGTTGACTATATGAGAGCTGTGAGATTTTATGATCCT 133

QY 21 GlnGluGlyTyrPheLysLeuAlaValAlaIleLysTyrProSerGlyAspAspArgTyr 40
 DB 134 CAAGAAGATGAGAAAGATTGAGCTGATTAATAAACCATCTGTGTGATGATGATAC 193

QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
 DB 194 AATCAGTTTCACATAGGAGATTGAGCATTTACTTCAAACTGAAAAAGTCCCATCTCT 253

QY 61 GluLeuLeuPheAspTyrGlyTyrThrAsnGlyThrValGlyAspLeuValAspLeu 80
 DB 254 GAATTACTGTTTACTGCGGACCAAAATTCGACAGTTGTGTGATCTTGTGATCTTTTG 313

QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
 DB 314 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTGTCTCCCAAGATGCTGTTCCC 367

RESULT 10
 AF155118 2817 bp mRNA linear PRI 05-JAN-2000
 LOCUS Homo sapiens putative protein kinase NY-REN-64 antigen mRNA,
 DEFINITION complete cds.
 ACCESSION AF155118
 VERSION AF155118.1 GI:5360130
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2817)
 Scallan,M.J., Jordan,J.D., Williamson,B., Stockert,E., Bander,N.H.,
 Jongeneel,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T.
 and Old,L.J.
 Antigens recognized by autologous antibody in patients with
 renal-cell carcinoma
 Int. J. Cancer 83 (4), 456-464 (1999)
 MEDLINE 99438124
 PUBMED 10508479
 JOURNAL 2 (bases 1 to 2817)
 Scallan,M.J., Jordan,J.D., Williamson,B., Stockert,E., Bander,N.H.,
 Jongeneel,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T.
 and Old,L.J.
 Direct Submission
 Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering
 Institute, 1275 York Ave, New York, NY 10021, USA
 TITLE location/Qualifiers
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 SDTFHRSFYEIKNTNNPDERPI SVGANGKSGEGRVYKGYANTTVAVKLAAM
 VDTTTERKKQPDDEIKYMAKQGNLVELGFSDDGDLCLVIVYMPGSLDLRLSC
 LDGTPPLSWNRCKTLAGGANGINFLHNHHIRDKANILDLDEAPFAKISDFGLAR
 ASERPAQIVMTSRIVGTAYMAPALRGEIIPKSDIVSFGVLLLEITGLPAVDNHR
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 HOLIQEMTAS"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Mismatches:	Indels:	Gaps:
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US-10-001-254-6 (1-98) x AF155118 (1-2817)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgTysLeuSerAspPheIleAspPro 20
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QY 21 GlnGluGlyTyrPheLysLeuAlaValAlaIleLysTyrProSerGlyAspAspArgTyr 40
 DB 134 CAAGAAGATGAGAAAGATTGAGCTGATTAATAAACCATCTGTGTGATGATGATAC 193

QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
 DB 194 AATCAGTTTCACATAGGAGATTGAGCATTTACTTCAAACTGAAAAAGTCCCATCTCT 253

QY 61 GluLeuLeuPheAspTyrGlyTyrThrAsnGlyThrValGlyAspLeuValAspLeu 80
 DB 254 GAATTACTGTTTACTGCGGACCAAAATTCGACAGTTGTGTGATCTTGTGATCTTTTG 313

QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
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RESULT 11
 AK000528 2820 bp mRNA linear PRI 13-SEP-2003
 LOCUS Homo sapiens cDNA FLJ20521 fls, clone KAT10395.
 DEFINITION AK000528
 ACCESSION AK000528
 VERSION AK000528.1 GI:7020683
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
 Ota,T., Suzuki,Y., Ohyashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
 Nakamura,T., Isogai,T. and Sugano,S.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2820)
 Sugano,S., Suzuki,Y., Ota,T., Ohyashi,M., Nishi,T., Isogai,T.,
 Shibahara,T., Tanaka,T. and Nakamura,Y.
 Direct Submission
 Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,
 Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp,
 Tel:81-3-5449-5286, Fax:81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry for Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library
 construction; 5' - & 3' -end one pass sequencing; Departent of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).
 TITLE location/Qualifiers
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VDITTEELKQFDQEIYKMAKQCHENIVELFSSDDDLCLVYVMPNGLDLRLSC
LDGTPPLSMWRCKIAQGAANGINFLNHHIHRDIIKSANILDEAFATKNSLDGLAR
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ORIGIN

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DB:	9	Gaps:	0

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QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgYsLeuSerAspPheIleAspPro 20
Db 54 ACATATGTGGCGCTCCCTCAATGTTGACTAATTAGGAAGCTGTGCAGATTTTATGATCCT 113
QY 21 GlnGlnGlyTTPlySylsLeuAlaValAlaIleYsYsProSerGlyAspAspArgTyr 40
Db 114 CAAGAAGATGAGAAAGTTAGCTGTACCTATTAACCAATCTGCGATGATGATAC 173
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyYsSerProThrSer 60
Db 174 AATCAGTTTCACATRAGAGATTGAGACATTACTCAATCGAAGAAAAGTCCCATCTCT 233
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCyThrValGlyAspLeuValAspLeu 80
Db 234 GAATTAAGTTTGTGACTGGGCGACCAAAATGACAGTGTGATCTTGATGATCTTTG 293
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 294 ATCCAAATGAATTTTGTCTCGCGAGCTTTTGTCTCCAGATGCTTCCC 347

RESULT 12

LOCUS AY283671 1381 bp mRNA linear PRI 17-JUN-2003
DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form
ACCESSION AY283671
VERSION AY283671.1 GI:31871819

KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Medvedev A.E., Lentschat A., Kuhns D.B., Bianco J.C.G.,
AUTHORS Salukowski C., Zhang S., Arditi M., Gallin J.I. and Vogel S.N.
TITLE Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
Bacterial Infections

J. Exp. Med. (2003) In press
2 (bases 1 to 1381)

JOURNAL Medvedev A.E., Lentschat A., Kuhns D.B., Bianco J.C.G.,
REFERENCE Salukowski C., Zhang S., Arditi M., Gallin J.I. and Vogel S.N.
AUTHORS Direct Submission
TITLE Submitted (25-APR-2003) Microbiology and Immunology, University of
JOURNAL Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD
21201-1559, USA

FEATURES

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of positions 620-621 in the wild-type coding region"

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LDGTPPLSMWRCKIAQGAANGINFLNHHIHRDIIKSANILDEAFATKNSLDGLAR
ASKEAQVTMTSRIVGTAVYAPALRGESITPKSDIYSGVLLLEITGLPQVNEHE
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variation

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ORIGIN

Alignment Scores:

Pred. No.:	3,246-60	Length:	1381
Score:	513.00	Matches:	97
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	9	Gaps:	0

US-10-001-254-6 (1-98) x AY283671 (1-1381)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgYsLeuSerAspPheIleAspPro 20
Db 25 ACATATGTGGCGCTCCCTCAATGTTGACTAATTAGGAAGCTGTGCAGATTTTATGATCCT 84
QY 21 GlnGlnGlyTTPlySylsLeuAlaValAlaIleYsYsProSerGlyAspAspArgTyr 40
Db 85 CAAGAAGATGAGAAAGTTAGCTGTACCTATTAACCAATCTGCGATGATGATAC 144
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyYsSerProThrSer 60
Db 145 AATCAGTTTCACATRAGAGATTGAGACATTACTCAATCGAAGAAAAGTCCCATCTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCyThrValGlyAspLeuValAspLeu 80
Db 205 GAATTAAGTTTGTGACTGGGCGACCAAAATGACAGTGTGATCTTGATGATCTTTG 264
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 265 ATCCAAATGAATTTTGTCTCGCGAGCTTTTGTCTCCAGATGCTTCCC 318

RESULT 13

LOCUS AX196260 1383 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 2 from Patent WO0151641.

ACCESSION AX196260
VERSION AX196260.1 GI:15386462

KEYWORDS

ORGANISM Homo sapiens (human)

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Wesche H. and Li S.
TITLE Irak-4: compositions and methods of use

JOURNAL Patent: WO 0151641-A 2 19-JUL-2001;
Tularik Inc. (US)
Location/Qualifiers
FEATURES
source

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VITTEELKQDFQDEIKVAKCQHENVLLGFSDDDLCLVYVYMPGSLIDRLSC
LDGTPPLSMHMRCKIAQGANGLFNHNNHHRDIKSNITLDEAFIAKISDFGLAR
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ORIGIN

Alignment Scores:

Pred. No.: 3,246-60 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AX196260 (1-1383)

QY 1 ThrTyrValArgCySeuAenValIGlyLeuIIearGlySeuSerAepPheIIeaAPro 20
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QY 21 GINGIUGIYTPDLYBLVLeuAlaValAlaIleIleYsPProSeRGIYAsPaPaRgTYr 40
DB 85 CAAAGAGATGAGAGAGATTAGCTGTAGCTATTAATAAACCACTGCTGATGATGATAC 144
QY 41 AengInPheHsiIleArgArpPheGluAlaLeuLeuInThrGlyYsSerProThrSer 60
DB 145 AATCGATTTCACATAGAGATTGAGACATTAATCAATCGAAGAAAGTCCCACTCTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThraSncCyThValGlyAspLeuValAspLeuLeu 80
DB 205 GAATTACGCTTTGACTGGGGCACACCAAAATTGACACGCTGGATCTTGGATCTTTTG 264
QY 81 IlegInaengIuphePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTTCCTCTCGAGATCTTTTCTCCAGATCTCTTCCC 318

RESULT 14
LOCUS AF445802 1383 bp mRNA linear PRI 20-APR-2002
DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4)
ACCESSION AF445802
VERSION AF445802.1 GI:20219009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Li S., Streteow, A., Fontana, E.J. and Wesche, H.
TITLE IRAK-4: a novel member of the IRAK family with the properties of an
IRAK-kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)
MEDLINE 21957277

PUBMED

11960013
2 (bases 1 to 1383)
REFERENCE Suzuki, N., Suzuki, S., Duncan, G.S., Miller, D.G., Wada, T.,
AUTHORS Mitsuo, C., Takada, H., Wakeham, A., Irie, A., Li, S., Penninger, J.M.,
TITLE Wesche, H., Ohashi, P.S., Mak, T.W., and Vell, W.C.
Severe impairment of interleukin-1 and Toll-like receptor
signaling in mice lacking IRAK-4
JOURNAL Nature 416 (6882), 750-756 (2002)
MEDLINE 21959395
11923871

PUBMED

3 (bases 1 to 1383)
REFERENCE Li, S., Streteow, A., Fontana, E.J. and Wesche, H.
AUTHORS Direct Submision
TITLE Submitted (08-NOV-2001) Biology I, Tularik Inc., 2 Corporate Drive,
JOURNAL South San Francisco, CA 94080, USA

FEATURES

source

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VITTEELKQDFQDEIKVAKCQHENVLLGFSDDDLCLVYVYMPGSLIDRLSC
LDGTPPLSMHMRCKIAQGANGLFNHNNHHRDIKSNITLDEAFIAKISDFGLAR
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CDS

gene

ORIGIN

Alignment Scores:

Pred. No.: 3,246-60 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AF445802 (1-1383)

QY 1 ThrTyrValArgCySeuAenValIGlyLeuIIearGlySeuSerAepPheIIeaAPro 20
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QY 21 GINGIUGIYTPDLYBLVLeuAlaValAlaIleIleYsPProSeRGIYAsPaPaRgTYr 40
DB 85 CAAAGAGATGAGAGATTAGCTGTAGCTATTAATAAACCACTGCTGATGATGATAC 144
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DB 205 GAATTACGCTTTGACTGGGGCACACCAAAATTGACACGCTGGATCTTGGATCTTTTG 264
QY 81 IlegInaengIuphePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTTCCTCTCGAGATCTTTTCTCCAGATCTCTTCCC 318

RESULT 15

LOCUS

AY283670 1383 bp mRNA linear PRI 17-JUN-2003

DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form
 1 (IRAK4) mRNA, complete cds.
 ACCESSION AY283670
 VERSION AY283670.1 GI:31871817
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Medvedev, A.E., Lentschat, A., Kuhns, D.B., Bianco, J.C.G., Salikowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N. Distinct mutations in IRAK-4 Confer Hyporesponsiveness to lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
 J. Exp. Med. (2003) In press
 JOURNAL 2 (bases 1 to 1383)
 REFERENCE Medvedev, A.E., Lentschat, A., Kuhns, D.B., Bianco, J.C.G., Salikowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N. Distinct mutations in IRAK-4 Confer Hyporesponsiveness to lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
 J. Exp. Med. (2003) In press
 TITLE Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA
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 ORIGIN
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 Pred. No.: 3.24e-60 Length: 1383
 Score: 513.00 Matches: 97
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 Best Local Similarity: 98.98% Mismatches: 1
 Query Match: 99.23% Indels: 0
 DB: 9 Gaps: 0
 US-10-001-254-6 (1-98) x AY283670 (1-1383)
 Qy 1 ThrTyrValaIrgCYsLeuAenValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 Db 25 ACATATGTGGCGCTCCATATGAGTAATTAAGAGAGCTGTGATTTATGATCTCT 84
 Qy 21 GlnGlnGlyTTrpIlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40

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 Db 145 AATCAGTTTCACATTAAGAGATTGAAGCACTTACTTCAAACTGAGAAAAAGTCCCATCTCT 204
 Qy 61 GlnLeuLeuPheAspTTrpGlyThrThrAsnCyThrValGlyAspLeuValAspLeuLeu 80
 Db 205 GAATTACTGTTTGACTGGGACACCAAAATGACAGCTGTATCTTGTGAGATCTTTG 264
 Qy 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 Db 265 ATCCAAATGAATTTTTCCTCTCCGAGCTTTTGTCTCCAGATGCTGTTCC 318

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